

SUBSTITUTE SEQUENCE LISTING

<110> Bihain, Bernard
 Bougueleret, Lydie
 Yen-Potin, Frances

<120> LSR Receptor, Its Activity, Its Cloning and Its Application To
 The Diagnosis Prevention And/or Treatment of Obesity and
 Related Risks or Complications

<130> GENSET.035APC

<150> FR 97/10088
 <151> 1997-08-06

<150> FR 98/05032
 <151> 1998-04-22

<160> 41

<170> Patent.pm

<210> 1
 <211> 2097
 <212> DNA
 <213> Rattus norvegicus

<400> 1
 accgctcacc aggtcagttg tccccggaaa gccgaaggca tgagcttcgc ccaagttctt 60
 tttatgggtt agaactcctc cagagcgggg gaaaaaggac ttggaatagg ggcgggacgg 120
 agcacgcacc cttctccgcc ttggttctcg ccgcgcccc tactctcggg atacttgga 180
 ggggacgcgc gggcaccgtc gctgctagac ggccgcg atg gcg ccg gcg gcc ggc 235
 Met Ala Pro Ala Ala Gly
 1 5
 gcg tgt gct ggg gcg cct gac tcc cac cca gct acc gtg gtc ttc gtg 283
 Ala Cys Ala Gly Ala Pro Asp Ser His Pro Ala Thr Val Val Phe Val
 10 15 20
 tgt ctc ttt ctc atc att ttc tgc cca gac cct gcc agt gcc atc cag 331
 Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp Pro Ala Ser Ala Ile Gln
 25 30 35
 gtg act gtg tct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg 379
 Val Thr Val Ser Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val
 40 45 50
 acc ctg ccc tgc acc tat cag atg agc aac act ctc aca gtc ccc atc 427
 Thr Leu Pro Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Val Pro Ile
 55 60 65 70
 gtg atc tgg aag tac aag tca ttc tgc cgg gac cgt att gcc gat gcc 475

Val	Ile	Trp	Lys	Tyr	Lys	Ser	Phe	Cys	Arg	Asp	Arg	Ile	Ala	Asp	Ala	
			75					80						85		
ttc	tct	cct	gcc	agt	gtg	gac	aac	cag	cta	aat	gcc	cag	ttg	gca	gct	523
Phe	Ser	Pro	Ala	Ser	Val	Asp	Asn	Gln	Leu	Asn	Ala	Gln	Leu	Ala	Ala	
			90					95					100			
ggc	aac	ccc	ggc	tac	aac	ccc	tat	gtg	gag	tgc	cag	gac	agt	gta	cgc	571
Gly	Asn	Pro	Gly	Tyr	Asn	Pro	Tyr	Val	Glu	Cys	Gln	Asp	Ser	Val	Arg	
		105					110					115				
act	gtc	agg	gtg	gtg	gcc	acc	aaa	cag	ggc	aat	gcg	gtg	acc	ctg	gga	619
Thr	Val	Arg	Val	Val	Ala	Thr	Lys	Gln	Gly	Asn	Ala	Val	Thr	Leu	Gly	
	120					125					130					
gac	tac	tac	caa	ggc	agg	agg	atc	acc	ata	aca	gga	aat	gct	gac	ctg	667
Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	Ile	Thr	Gly	Asn	Ala	Asp	Leu	
135					140				145						150	
acc	ttc	gag	cag	aca	gcc	tgg	gga	gac	agt	gga	gtg	tat	tac	tgc	tct	715
Thr	Phe	Glu	Gln	Thr	Ala	Trp	Gly	Asp	Ser	Gly	Val	Tyr	Tyr	Cys	Ser	
				155				160						165		
gtg	gtc	tcg	gcc	caa	gat	ctg	gat	gga	aac	aac	gag	gcg	tac	gca	gag	763
Val	Val	Ser	Ala	Gln	Asp	Leu	Asp	Gly	Asn	Asn	Glu	Ala	Tyr	Ala	Glu	
			170					175					180			
ctc	atc	gtc	ctt	ggc	agg	acc	tca	gag	gcc	cct	gag	ctc	cta	cct	ggt	811
Leu	Ile	Val	Leu	Gly	Arg	Thr	Ser	Glu	Ala	Pro	Glu	Leu	Leu	Pro	Gly	
		185					190					195				
ttt	cgg	gcg	ggg	ccc	ttg	gaa	gat	tgg	ctc	ttt	gtg	gtc	gtg	gtc	tgc	859
Phe	Arg	Ala	Gly	Pro	Leu	Glu	Asp	Trp	Leu	Phe	Val	Val	Val	Val	Cys	
	200					205					210					
ctg	gcg	agc	ctc	ctc	ctc	ttc	ctc	ctc	ctg	ggc	atc	tgc	tgg	tgc	cag	907
Leu	Ala	Ser	Leu	Leu	Leu	Phe	Leu	Leu	Leu	Gly	Ile	Cys	Trp	Cys	Gln	
215					220					225					230	
tgc	tgt	cct	cac	acc	tgc	tgc	tgc	tat	gtc	cga	tgt	ccc	tgc	tgc	cca	955
Cys	Cys	Pro	His	Thr	Cys	Cys	Cys	Tyr	Val	Arg	Cys	Pro	Cys	Cys	Pro	
				235				240						245		
gac	aag	tgc	tgt	tgc	cct	gag	gct	ctt	tat	gct	gct	ggc	aaa	gca	gcc	1003
Asp	Lys	Cys	Cys	Cys	Pro	Glu	Ala	Leu	Tyr	Ala	Ala	Gly	Lys	Ala	Ala	
			250					255					260			
acc	tca	ggt	gtc	ccg	agc	atc	tat	gcc	ccc	agc	atc	tat	acc	cac	ctc	1051
Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Ile	Tyr	Thr	His	Leu	
		265					270					275				
tca	cct	gcc	aag	acc	cca	cca	cct	ccg	cct	gcc	atg	att	ccc	atg	ggc	1099
Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro	Pro	Pro	Ala	Met	Ile	Pro	Met	Gly	
	280					285					290					
cct	ccc	tat	ggg	tac	cct	gga	gac	ttt	gac	aga	cat	agc	tca	gtt	ggt	1147
Pro	Pro	Tyr	Gly	Tyr	Pro	Gly	Asp	Phe	Asp	Arg	His	Ser	Ser	Val	Gly	

295		300		305		310	
ggc cac agc tcc caa gta ccc ctg ctg cgt gac gtg gat ggc agt gta	Gly His Ser Ser Gln Val Pro Leu Leu Arg Asp Val Asp Gly Ser Val	1195					
	315 320 325						
tct tca gaa gta cga agt ggc tac agg atc cag gct aac cag caa gat	Ser Ser Glu Val Arg Ser Gly Tyr Arg Ile Gln Ala Asn Gln Gln Asp	1243					
	330 335 340						
gac tcc atg agg gtc cta tac tat atg gag aaa gag cta gcc aac ttt	Asp Ser Met Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe	1291					
	345 350 355						
gac cct tcc cga cct ggc cct ccc aat ggc aga gtg gaa cgg gcc atg	Asp Pro Ser Arg Pro Gly Pro Pro Asn Gly Arg Val Glu Arg Ala Met	1339					
	360 365 370						
agt gaa gta acc tcc ctc cat gaa gat gac tgg cga tcg agg cct tcc	Ser Glu Val Thr Ser Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser	1387					
	375 380 385 390						
agg gct cct gcc ctc acc ccc atc agg gat gag gag tgg aat cgc cac	Arg Ala Pro Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp Asn Arg His	1435					
	395 400 405						
tcc cca cag agt ccc aga aca tgg gag cag gaa ccc ctt caa gaa caa	Ser Pro Gln Ser Pro Arg Thr Trp Glu Gln Glu Pro Leu Gln Glu Gln	1483					
	410 415 420						
cca agg ggt ggt tgg ggg tct gga cgc cct cgg gcc cgc tct gtg gat	Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro Arg Ala Arg Ser Val Asp	1531					
	425 430 435						
gct cta gat gat atc aac cgg cct ggc tcc act gaa tca gga cgg tct	Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser Thr Glu Ser Gly Arg Ser	1579					
	440 445 450						
tct ccc cca agt agt gga cgg aga gga cgg gcc tat gca cct cca aga	Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg Ala Tyr Ala Pro Pro Arg	1627					
	455 460 465 470						
agt cgc agc cgg gat gac ctc tat gac ccg gac gat cct agg gac ttg	Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro Asp Asp Pro Arg Asp Leu	1675					
	475 480 485						
cca cat tcc cga gat ccc cac tat tat gac gac atc agg tct aga gat	Pro His Ser Arg Asp Pro His Tyr Tyr Asp Asp Ile Arg Ser Arg Asp	1723					
	490 495 500						
cca cgt gct gac ccc aga tcc cgt cag cga tcc cga gat cct cgg gat	Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg Ser Arg Asp Pro Arg Asp	1771					
	505 510 515						
gct ggc ttc agg tca agg gac cct cag tat gat ggg cga cta tta gaa	Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr Asp Gly Arg Leu Leu Glu	1819					
	520 525 530						

gag gct tta aag aaa aag ggg tcg ggc gag aga agg agg gtt tac agg	1867
Glu Ala Leu Lys Lys Lys Gly Ser Gly Glu Arg Arg Arg Val Tyr Arg	
535 540 545 550	
gag gaa gaa gag gaa gag gag ggc caa tac ccc cca gca cct cca cct	1915
Glu Glu Glu Glu Glu Glu Glu Gly Gln Tyr Pro Pro Ala Pro Pro Pro	
555 560 565	
tac tca gag act gac tcg cag gcc tca cgg gag agg agg ctg aaa aag	1963
Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys	
570 575 580	
aat ttg gcc ctg agt cgg gaa agt tta gtc gtc tga tccacgtttt	2009
Asn Leu Ala Leu Ser Arg Glu Ser Leu Val Val *	
585 590	
gtatgtagct tttgtacttt ttttttaatt ggaatcaata ttgatgaaac ttcaagccta	2069
ataaaatgtc taatcacaaa aaaaaaaaaa	2097

<210> 2
 <211> 593
 <212> PRT
 <213> Rattus norvegicus

<400> 2															
Met	Ala	Pro	Ala	Ala	Gly	Ala	Cys	Ala	Gly	Ala	Pro	Asp	Ser	His	Pro
1				5					10					15	
Ala	Thr	Val	Val	Phe	Val	Cys	Leu	Phe	Leu	Ile	Ile	Phe	Cys	Pro	Asp
			20					25					30		
Pro	Ala	Ser	Ala	Ile	Gln	Val	Thr	Val	Ser	Asp	Pro	Tyr	His	Val	Val
		35					40					45			
Ile	Leu	Phe	Gln	Pro	Val	Thr	Leu	Pro	Cys	Thr	Tyr	Gln	Met	Ser	Asn
	50					55					60				
Thr	Leu	Thr	Val	Pro	Ile	Val	Ile	Trp	Lys	Tyr	Lys	Ser	Phe	Cys	Arg
65					70					75					80
Asp	Arg	Ile	Ala	Asp	Ala	Phe	Ser	Pro	Ala	Ser	Val	Asp	Asn	Gln	Leu
				85					90					95	
Asn	Ala	Gln	Leu	Ala	Ala	Gly	Asn	Pro	Gly	Tyr	Asn	Pro	Tyr	Val	Glu
			100					105					110		
Cys	Gln	Asp	Ser	Val	Arg	Thr	Val	Arg	Val	Val	Ala	Thr	Lys	Gln	Gly
		115					120					125			
Asn	Ala	Val	Thr	Leu	Gly	Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	Ile
	130					135					140				
Thr	Gly	Asn	Ala	Asp	Leu	Thr	Phe	Glu	Gln	Thr	Ala	Trp	Gly	Asp	Ser

145		150		155		160
Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Asp Gly Asn	165		170		175	
Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Gly Arg Thr Ser Glu Ala	180		185		190	
Pro Glu Leu Leu Pro Gly Phe Arg Ala Gly Pro Leu Glu Asp Trp Leu	195		200		205	
Phe Val Val Val Val Cys Leu Ala Ser Leu Leu Leu Phe Leu Leu Leu	210		215		220	
Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr Cys Cys Cys Tyr Val	225		230		235	240
Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Cys Pro Glu Ala Leu Tyr	245		250		255	
Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro	260		265		270	
Ser Ile Tyr Thr His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro Pro	275		280		285	
Ala Met Ile Pro Met Gly Pro Pro Tyr Gly Tyr Pro Gly Asp Phe Asp	290		295		300	
Arg His Ser Ser Val Gly Gly His Ser Ser Gln Val Pro Leu Leu Arg	305		310		315	320
Asp Val Asp Gly Ser Val Ser Ser Glu Val Arg Ser Gly Tyr Arg Ile	325		330		335	
Gln Ala Asn Gln Gln Asp Asp Ser Met Arg Val Leu Tyr Tyr Met Glu	340		345		350	
Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro Pro Asn Gly	355		360		365	
Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser Leu His Glu Asp Asp	370		375		380	
Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala Leu Thr Pro Ile Arg Asp	385		390		395	400
Glu Glu Trp Asn Arg His Ser Pro Gln Ser Pro Arg Thr Trp Glu Gln	405		410		415	
Glu Pro Leu Gln Glu Gln Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro	420		425		430	
Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser	435		440		445	
Thr Glu Ser Gly Arg Ser Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg						

450	455	460
Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro		
465	470	475 480
Asp Asp Pro Arg Asp Leu Pro His Ser Arg Asp Pro His Tyr Tyr Asp		
	485	490 495
Asp Ile Arg Ser Arg Asp Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg		
	500	505 510
Ser Arg Asp Pro Arg Asp Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr		
	515	520 525
Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys Lys Lys Gly Ser Gly Glu		
	530	535 540
Arg Arg Arg Val Tyr Arg Glu Glu Glu Glu Glu Glu Gly Gln Tyr		
	545	550 555 560
Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg		
	565	570 575
Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val		
	580	585 590

Val

<210> 3
 <211> 2040
 <212> DNA
 <213> Rattus norvegicus

<400> 3

accgctcacc aggtcagttg tccccggaaa gccgaaggca tgagcttcgc ccaagttctt	60
tttatggggtt agaactcctc cagagcgggg gaaaaaggac ttggaatagg ggcgggacgg	120
agcacgcacc cttctccgcc ttggttctcg ccgcgcccc tactctcggg atacttgga	180
ggggacgcgc gggcaccgtc gctgctagac ggccgcg atg gcg ccg gcg gcc ggc	235
Met Ala Pro Ala Ala Gly	
1 5	
gcg tgt gct ggg gcg cct gac tcc cac cca gct acc gtg gtc ttc gtg	283
Ala Cys Ala Gly Ala Pro Asp Ser His Pro Ala Thr Val Val Phe Val	
10 15 20	
tgt ctc ttt ctc atc att ttc tgc cca gac cct gcc agt gcc atc cag	331
Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp Pro Ala Ser Ala Ile Gln	
25 30 35	
gtg act gtg tct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg	379
Val Thr Val Ser Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val	
40 45 50	
acc ctg ccc tgc acc tat cag atg agc aac act ctc aca gtc ccc atc	427

Thr 55	Leu	Pro	Cys	Thr 60	Tyr	Gln	Met	Ser	Asn 65	Thr	Leu	Thr	Val	Pro	Ile 70	
gtg	atc	tgg	aag	tac	aag	tca	ttc	tgc	cgg	gac	cgt	att	gcc	gat	gcc	475
Val	Ile	Trp	Lys	Tyr 75	Lys	Ser	Phe	Cys	Arg 80	Asp	Arg	Ile	Ala	Asp	Ala	
ttc	tct	cct	gcc	agt	gtg	gac	aac	cag	cta	aat	gcc	cag	ttg	gca	gct	523
Phe	Ser	Pro	Ala 90	Ser	Val	Asp	Asn	Gln 95	Leu	Asn	Ala	Gln	Leu	Ala	Ala	
ggc	aac	ccc	ggc	tac	aac	ccc	tat	gtg	gag	tgc	cag	gac	agt	gta	cgc	571
Gly	Asn	Pro 105	Gly	Tyr	Asn	Pro	Tyr 110	Val	Glu	Cys	Gln	Asp	Ser	Val	Arg	
act	gtc	agg	gtg	gtg	gcc	acc	aaa	cag	ggc	aat	gcg	gtg	acc	ctg	gga	619
Thr	Val	Arg	Val	Val	Ala	Thr 120	Lys 125	Gln	Gly	Asn	Ala 130	Val	Thr	Leu	Gly	
gac	tac	tac	caa	ggc	agg	agg	atc	acc	ata	aca	gga	aat	gct	gac	ctg	667
Asp	Tyr	Tyr	Gln	Gly	Arg 135	Arg	Ile 140	Thr	Ile	Thr 145	Gly	Asn	Ala	Asp	Leu	
acc	ttc	gag	cag	aca	gcc	tgg	gga	gac	agt	gga	gtg	tat	tac	tgc	tct	715
Thr	Phe	Glu	Gln	Thr 155	Ala	Trp	Gly	Asp	Ser 160	Gly	Val	Tyr	Tyr	Cys	Ser	
gtg	gtc	tcg	gcc	caa	gat	ctg	gat	gga	aac	aac	gag	gcg	tac	gca	gag	763
Val	Val	Ser	Ala 170	Gln	Asp	Leu	Asp	Gly 175	Asn	Asn	Glu	Ala	Tyr	Ala	Glu	
ctc	atc	gtc	ctt	gat	tgg	ctc	ttt	gtg	gtc	gtg	gtc	tgc	ctg	gcg	agc	811
Leu	Ile	Val 185	Leu	Asp	Trp	Leu	Phe 190	Val	Val	Val	Val	Cys	Leu	Ala	Ser	
ctc	ctc	ctc	ttc	ctc	ctc	ctg	ggc	atc	tgc	tgg	tgc	cag	tgc	tgt	cct	859
Leu	Leu	Leu 200	Phe	Leu	Leu	Leu 205	Gly	Ile	Cys	Trp	Cys	Gln	Cys	Cys	Pro	
cac	acc	tgc	tgc	tgc	tat	gtc	cga	tgt	ccc	tgc	tgc	cca	gac	aag	tgc	907
His	Thr	Cys	Cys	Cys	Tyr 215	Val	Arg	Cys	Pro	Cys 225	Cys	Pro	Asp	Lys	Cys	
tgt	tgc	cct	gag	gct	ctt	tat	gct	gct	ggc	aaa	gca	gcc	acc	tca	ggc	955
Cys	Cys	Pro	Glu	Ala 235	Leu	Tyr	Ala	Ala	Gly 240	Lys	Ala	Ala	Thr	Ser	Gly	
gtc	ccg	agc	atc	tat	gcc	ccc	agc	atc	tat	acc	cac	ctc	tca	cct	gcc	1003
Val	Pro	Ser	Ile	Tyr	Ala 250	Pro	Ser	Ile	Tyr	Thr	His	Leu	Ser	Pro	Ala	
aag	acc	cca	cca	cct	ccg	cct	gcc	atg	att	ccc	atg	ggc	cct	ccc	tat	1051
Lys	Thr	Pro 265	Pro	Pro	Pro	Pro	Ala 270	Met	Ile	Pro	Met	Gly	Pro	Pro	Tyr	
ggg	tac	cct	gga	gac	ttt	gac	aga	cat	agc	tca	gtt	ggc	ggc	cac	agc	1099
Gly	Tyr	Pro	Gly	Asp	Phe	Asp	Arg	His	Ser	Ser	Val	Gly	Gly	His	Ser	

280	285	290	
tcc caa gta ccc ctg ctg cgt gac gtg gat ggc agt gta tct tca gaa Ser Gln Val Pro Leu Leu Arg Asp Val Asp Gly Ser Val Ser Ser Glu 295 300 305 310			1147
gta cga agt ggc tac agg atc cag gct aac cag caa gat gac tcc atg Val Arg Ser Gly Tyr Arg Ile Gln Ala Asn Gln Gln Asp Asp Ser Met 315 320 325			1195
agg gtc cta tac tat atg gag aaa gag cta gcc aac ttt gac cct tcc Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser 330 335 340			1243
cga cct ggc cct ccc aat ggc aga gtg gaa cgg gcc atg agt gaa gta Arg Pro Gly Pro Pro Asn Gly Arg Val Glu Arg Ala Met Ser Glu Val 345 350 355			1291
acc tcc ctc cat gaa gat gac tgg cga tcg agg cct tcc agg gct cct Thr Ser Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro 360 365 370			1339
gcc ctc acc ccc atc agg gat gag gag tgg aat cgc cac tcc cca cag Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp Asn Arg His Ser Pro Gln 375 380 385 390			1387
agt ccc aga aca tgg gag cag gaa ccc ctt caa gaa caa cca agg ggt Ser Pro Arg Thr Trp Glu Gln Glu Pro Leu Gln Glu Gln Pro Arg Gly 395 400 405			1435
ggt tgg ggg tct gga cgc cct cgg gcc cgc tct gtg gat gct cta gat Gly Trp Gly Ser Gly Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp 410 415 420			1483
gat atc aac cgg cct ggc tcc act gaa tca gga cgg tct tct ccc cca Asp Ile Asn Arg Pro Gly Ser Thr Glu Ser Gly Arg Ser Ser Pro Pro 425 430 435			1531
agt agt gga cgg aga gga cgg gcc tat gca cct cca aga agt cgc agc Ser Ser Gly Arg Arg Gly Arg Ala Tyr Ala Pro Pro Arg Ser Arg Ser 440 445 450			1579
cgg gat gac ctc tat gac ccg gac gat cct agg gac ttg cca cat tcc Arg Asp Asp Leu Tyr Asp Pro Asp Asp Pro Arg Asp Leu Pro His Ser 455 460 465 470			1627
cga gat ccc cac tat tat gac gac atc agg tct aga gat cca cgt gct Arg Asp Pro His Tyr Tyr Asp Asp Ile Arg Ser Arg Asp Pro Arg Ala 475 480 485			1675
gac ccc aga tcc cgt cag cga tcc cga gat cct cgg gat gct ggc ttc Asp Pro Arg Ser Arg Gln Arg Ser Arg Asp Pro Arg Asp Ala Gly Phe 490 495 500			1723
agg tca agg gac cct cag tat gat ggg cga cta tta gaa gag gct tta Arg Ser Arg Asp Pro Gln Tyr Asp Gly Arg Leu Leu Glu Glu Ala Leu 505 510 515			1771

aag aaa aag ggg tcg ggc gag aga agg agg gtt tac agg gag gaa gaa	1819
Lys Lys Lys Gly Ser Gly Glu Arg Arg Arg Val Tyr Arg Glu Glu Glu	
520 525 530	
gag gaa gag gag ggc caa tac ccc cca gca cct cca cct tac tca gag	1867
Glu Glu Glu Glu Gly Gln Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu	
535 540 545 550	
act gac tcg cag gcc tca cgg gag agg agg ctg aaa aag aat ttg gcc	1915
Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala	
555 560 565	
ctg agt cgg gaa agt tta gtc gtc tga tccacgtttt gtatgtagct	1962
Leu Ser Arg Glu Ser Leu Val Val *	
570	
tttgtacttt ttttttaatt ggaatcaata ttgatgaaac ttcaagccta ataaaatgtc	2022
taatcacaaa aaaaaaaaa	2040

<210> 4
 <211> 574
 <212> PRT
 <213> Rattus norvegicus

<400> 4	
Met Ala Pro Ala Ala Gly Ala Cys Ala Gly Ala Pro Asp Ser His Pro	
1 5 10 15	
Ala Thr Val Val Phe Val Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp	
20 25 30	
Pro Ala Ser Ala Ile Gln Val Thr Val Ser Asp Pro Tyr His Val Val	
35 40 45	
Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Ser Asn	
50 55 60	
Thr Leu Thr Val Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg	
65 70 75 80	
Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu	
85 90 95	
Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu	
100 105 110	
Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly	
115 120 125	
Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile	
130 135 140	
Thr Gly Asn Ala Asp Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser	
145 150 155 160	

Gly	Val	Tyr	Tyr	Cys	Ser	Val	Val	Ser	Ala	Gln	Asp	Leu	Asp	Gly	Asn	
				165					170					175		
Asn	Glu	Ala	Tyr	Ala	Glu	Leu	Ile	Val	Leu	Asp	Trp	Leu	Phe	Val	Val	
			180					185					190			
Val	Val	Cys	Leu	Ala	Ser	Leu	Leu	Leu	Phe	Leu	Leu	Leu	Gly	Ile	Cys	
		195					200					205				
Trp	Cys	Gln	Cys	Cys	Pro	His	Thr	Cys	Cys	Cys	Tyr	Val	Arg	Cys	Pro	
	210					215					220					
Cys	Cys	Pro	Asp	Lys	Cys	Cys	Cys	Pro	Glu	Ala	Leu	Tyr	Ala	Ala	Gly	
225					230					235					240	
Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Ile	Tyr	
				245					250					255		
Thr	His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro	Pro	Pro	Ala	Met	Ile	
			260					265					270			
Pro	Met	Gly	Pro	Pro	Tyr	Gly	Tyr	Pro	Gly	Asp	Phe	Asp	Arg	His	Ser	
		275					280					285				
Ser	Val	Gly	Gly	His	Ser	Ser	Gln	Val	Pro	Leu	Leu	Arg	Asp	Val	Asp	
	290					295					300					
Gly	Ser	Val	Ser	Ser	Glu	Val	Arg	Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Asn	
305					310					315					320	
Gln	Gln	Asp	Asp	Ser	Met	Arg	Val	Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	
				325					330					335		
Ala	Asn	Phe	Asp	Pro	Ser	Arg	Pro	Gly	Pro	Pro	Asn	Gly	Arg	Val	Glu	
			340					345					350			
Arg	Ala	Met	Ser	Glu	Val	Thr	Ser	Leu	His	Glu	Asp	Asp	Trp	Arg	Ser	
		355					360					365				
Arg	Pro	Ser	Arg	Ala	Pro	Ala	Leu	Thr	Pro	Ile	Arg	Asp	Glu	Glu	Trp	
	370					375					380					
Asn	Arg	His	Ser	Pro	Gln	Ser	Pro	Arg	Thr	Trp	Glu	Gln	Glu	Pro	Leu	
385					390					395					400	
Gln	Glu	Gln	Pro	Arg	Gly	Gly	Trp	Gly	Ser	Gly	Arg	Pro	Arg	Ala	Arg	
			405					410						415		
Ser	Val	Asp	Ala	Leu	Asp	Asp	Ile	Asn	Arg	Pro	Gly	Ser	Thr	Glu	Ser	
			420				425						430			
Gly	Arg	Ser	Ser	Pro	Pro	Ser	Ser	Gly	Arg	Arg	Gly	Arg	Ala	Tyr	Ala	
		435				440					445					
Pro	Pro	Arg	Ser	Arg	Ser	Arg	Asp	Asp	Leu	Tyr	Asp	Pro	Asp	Asp	Pro	
	450					455					460					

Arg Asp Leu Pro His Ser Arg Asp Pro His Tyr Tyr Asp Asp Ile Arg
 465 470 475 480
 Ser Arg Asp Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg Ser Arg Asp
 485 490 495
 Pro Arg Asp Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr Asp Gly Arg
 500 505 510
 Leu Leu Glu Glu Ala Leu Lys Lys Lys Gly Ser Gly Glu Arg Arg Arg
 515 520 525
 Val Tyr Arg Glu Glu Glu Glu Glu Glu Gly Gln Tyr Pro Pro Ala
 530 535 540
 Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg
 545 550 555 560
 Leu Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val Val
 565 570

<210> 5
 <211> 1893
 <212> DNA
 <213> Rattus norvegicus

<400> 5
 accgctcacc aggtcagttg tccccggaaa gccgaaggca tgagcttcgc ccaagttctt 60
 tttatggggtt agaactcctc cagagcgggg gaaaaaggac ttggaatagg ggcgggacgg 120
 agcacgcacc cttctccgcc ttggttctcg ccgcgcccc tactctcggg atacttggga 180
 ggggacgcgc gggcaccgtc gctgctagac ggccgcg atg gcg ccg gcg gcc ggc 235
 Met Ala Pro Ala Ala Gly
 1 5
 gcg tgt gct ggg gcg cct gac tcc cac cca gct acc gtg gtc ttc gtg 283
 Ala Cys Ala Gly Ala Pro Asp Ser His Pro Ala Thr Val Val Phe Val
 10 15 20
 tgt ctc ttt ctc atc att ttc tgc cca gac cct gcc agt gcc atc cag 331
 Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp Pro Ala Ser Ala Ile Gln
 25 30 35
 gtg act gtg tct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg 379
 Val Thr Val Ser Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val
 40 45 50
 acc ctg ccc tgc acc tat cag atg agc aac act ctc aca gtc ccc atc 427
 Thr Leu Pro Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Val Pro Ile
 55 60 65 70
 gtg atc tgg aag tac aag tca ttc tgc cgg gac cgt att gcc gat gcc 475
 Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg Asp Arg Ile Ala Asp Ala

75						80						85						
ttc	tct	cct	gcc	agt	gtg	gac	aac	cag	cta	aat	gcc	cag	ttg	gca	gct	523		
Phe	Ser	Pro	Ala	Ser	Val	Asp	Asn	Gln	Leu	Asn	Ala	Gln	Leu	Ala	Ala			
			90					95					100					
ggc	aac	ccc	ggc	tac	aac	ccc	tat	gtg	gag	tgc	cag	gac	agt	gta	cgc	571		
Gly	Asn	Pro	Gly	Tyr	Asn	Pro	Tyr	Val	Glu	Cys	Gln	Asp	Ser	Val	Arg			
		105					110					115						
act	gtc	agg	gtg	gtg	gcc	acc	aaa	cag	ggc	aat	gcg	gtg	acc	ctg	gga	619		
Thr	Val	Arg	Val	Val	Ala	Thr	Lys	Gln	Gly	Asn	Ala	Val	Thr	Leu	Gly			
	120					125					130							
gac	tac	tac	caa	ggc	agg	agg	atc	acc	ata	aca	gga	aat	gct	gac	ctg	667		
Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	Ile	Thr	Gly	Asn	Ala	Asp	Leu			
135					140					145					150			
acc	ttc	gag	cag	aca	gcc	tgg	gga	gac	agt	gga	gtg	tat	tac	tgc	tct	715		
Thr	Phe	Glu	Gln	Thr	Ala	Trp	Gly	Asp	Ser	Gly	Val	Tyr	Tyr	Cys	Ser			
				155				160						165				
gtg	gtc	tcg	gcc	caa	gat	ctg	gat	gga	aac	aac	gag	gcg	tac	gca	gag	763		
Val	Val	Ser	Ala	Gln	Asp	Leu	Asp	Gly	Asn	Asn	Glu	Ala	Tyr	Ala	Glu			
			170					175					180					
ctc	atc	gtc	ctt	gtt	tat	gct	gct	ggc	aaa	gca	gcc	acc	tca	ggg	gtc	811		
Leu	Ile	Val	Leu	Val	Tyr	Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser	Gly	Val			
		185				190						195						
ccg	agc	atc	tat	gcc	ccc	agc	atc	tat	acc	cac	ctc	tca	cct	gcc	aag	859		
Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Ile	Tyr	Thr	His	Leu	Ser	Pro	Ala	Lys			
	200					205					210							
acc	cca	cca	cct	ccg	cct	gcc	atg	att	ccc	atg	ggc	cct	ccc	tat	ggg	907		
Thr	Pro	Pro	Pro	Pro	Pro	Ala	Met	Ile	Pro	Met	Gly	Pro	Pro	Tyr	Gly			
215					220				225					230				
tac	cct	gga	gac	ttt	gac	aga	cat	agc	tca	gtt	ggg	ggc	cac	agc	tcc	955		
Tyr	Pro	Gly	Asp	Phe	Asp	Arg	His	Ser	Ser	Val	Gly	Gly	His	Ser	Ser			
				235				240						245				
caa	gta	ccc	ctg	ctg	cgt	gac	gtg	gat	ggc	agt	gta	tct	tca	gaa	gta	1003		
Gln	Val	Pro	Leu	Leu	Arg	Asp	Val	Asp	Gly	Ser	Val	Ser	Ser	Glu	Val			
			250					255					260					
cga	agt	ggc	tac	agg	atc	cag	gct	aac	cag	caa	gat	gac	tcc	atg	agg	1051		
Arg	Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Asn	Gln	Gln	Asp	Asp	Ser	Met	Arg			
		265				270						275						
gtc	cta	tac	tat	atg	gag	aaa	gag	cta	gcc	aac	ttt	gac	cct	tcc	cga	1099		
Val	Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser	Arg			
	280					285					290							
cct	ggc	cct	ccc	aat	ggc	aga	gtg	gaa	cgg	gcc	atg	agt	gaa	gta	acc	1147		
Pro	Gly	Pro	Pro	Asn	Gly	Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val	Thr			
295					300					305					310			

tcc ctc cat gaa gat gac tgg cga tcg agg cct tcc agg gct cct gcc	1195
Ser Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala	
315 320 325	
ctc acc ccc atc agg gat gag gag tgg aat cgc cac tcc cca cag agt	1243
Leu Thr Pro Ile Arg Asp Glu Glu Trp Asn Arg His Ser Pro Gln Ser	
330 335 340	
ccc aga aca tgg gag cag gaa ccc ctt caa gaa caa cca agg ggt ggt	1291
Pro Arg Thr Trp Glu Gln Glu Pro Leu Gln Glu Gln Pro Arg Gly Gly	
345 350 355	
tgg ggg tct gga cgc cct cgg gcc cgc tct gtg gat gct cta gat gat	1339
Trp Gly Ser Gly Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp	
360 365 370	
atc aac cgg cct ggc tcc act gaa tca gga cgg tct tct ccc cca agt	1387
Ile Asn Arg Pro Gly Ser Thr Glu Ser Gly Arg Ser Ser Pro Pro Ser	
375 380 385 390	
agt gga cgg aga gga cgg gcc tat gca cct cca aga agt cgc agc cgg	1435
Ser Gly Arg Arg Gly Arg Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg	
395 400 405	
gat gac ctc tat gac ccg gac gat cct agg gac ttg cca cat tcc cga	1483
Asp Asp Leu Tyr Asp Pro Asp Asp Pro Arg Asp Leu Pro His Ser Arg	
410 415 420	
gat ccc cac tat tat gac gac atc agg tct aga gat cca cgt gct gac	1531
Asp Pro His Tyr Tyr Asp Asp Ile Arg Ser Arg Asp Pro Arg Ala Asp	
425 430 435	
ccc aga tcc cgt cag cga tcc cga gat cct cgg gat gct ggc ttc agg	1579
Pro Arg Ser Arg Gln Arg Ser Arg Asp Pro Arg Asp Ala Gly Phe Arg	
440 445 450	
tca agg gac cct cag tat gat ggg cga cta tta gaa gag gct tta aag	1627
Ser Arg Asp Pro Gln Tyr Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys	
455 460 465 470	
aaa aag ggg tcg ggc gag aga agg agg gtt tac agg gag gaa gaa gag	1675
Lys Lys Gly Ser Gly Glu Arg Arg Arg Val Tyr Arg Glu Glu Glu Glu	
475 480 485	
gaa gag gag ggc caa tac ccc cca gca cct cca cct tac tca gag act	1723
Glu Glu Glu Gly Gln Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr	
490 495 500	
gac tcg cag gcc tca cgg gag agg agg ctg aaa aag aat ttg gcc ctg	1771
Asp Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu	
505 510 515	
agt cgg gaa agt tta gtc gtc tga tccacgtttt gtatgtagct tttgtacttt	1825
Ser Arg Glu Ser Leu Val Val *	

520

525

ttttttaatt ggaatcaata ttgatgaaac ttcaagccta ataaaatgtc taatcacaaa 1885

aaaaaaaaa 1893

<210> 6

<211> 525

<212> PRT

<213> Rattus norvegicus

<400> 6

Met Ala Pro Ala Ala Gly Ala Cys Ala Gly Ala Pro Asp Ser His Pro
1 5 10 15

Ala Thr Val Val Phe Val Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp
20 25 30

Pro Ala Ser Ala Ile Gln Val Thr Val Ser Asp Pro Tyr His Val Val
35 40 45

Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Ser Asn
50 55 60

Thr Leu Thr Val Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg
65 70 75 80

Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu
85 90 95

Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu
100 105 110

Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly
115 120 125

Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile
130 135 140

Thr Gly Asn Ala Asp Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser
145 150 155 160

Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Asp Gly Asn
165 170 175

Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Val Tyr Ala Ala Gly Lys
180 185 190

Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro Ser Ile Tyr Thr
195 200 205

His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro Pro Ala Met Ile Pro
210 215 220

Met Gly Pro Pro Tyr Gly Tyr Pro Gly Asp Phe Asp Arg His Ser Ser

225		230		235		240
Val Gly Gly His	Ser Ser Gln Val	Pro Leu Leu Arg	Asp Val Asp Gly			
	245		250		255	
Ser Val Ser Ser	Glu Val Arg Ser	Gly Tyr Arg Ile	Gln Ala Asn Gln			
	260	265	270			
Gln Asp Asp Ser	Met Arg Val Leu	Tyr Tyr Met Glu	Lys Glu Leu Ala			
	275	280	285			
Asn Phe Asp Pro	Ser Arg Pro Gly	Pro Pro Asn Gly	Arg Val Glu Arg			
	290	295	300			
Ala Met Ser Glu	Val Thr Ser Leu	His Glu Asp Asp	Trp Arg Ser Arg			
305	310	315	320			
Pro Ser Arg Ala	Pro Ala Leu Thr	Pro Ile Arg Asp	Glu Glu Trp Asn			
	325	330	335			
Arg His Ser Pro	Gln Ser Pro Arg	Thr Trp Glu Gln	Glu Pro Leu Gln			
	340	345	350			
Glu Gln Pro Arg	Gly Gly Trp Gly	Ser Gly Arg Pro	Arg Ala Arg Ser			
	355	360	365			
Val Asp Ala Leu	Asp Asp Ile Asn	Arg Pro Gly Ser	Thr Glu Ser Gly			
	370	375	380			
Arg Ser Ser Pro	Pro Ser Ser Gly	Arg Arg Gly Arg	Ala Tyr Ala Pro			
385	390	395	400			
Pro Arg Ser Arg	Ser Arg Asp Asp	Leu Tyr Asp Pro	Asp Asp Pro Arg			
	405	410	415			
Asp Leu Pro His	Ser Arg Asp Pro	His Tyr Tyr Asp	Asp Ile Arg Ser			
	420	425	430			
Arg Asp Pro Arg	Ala Asp Pro Arg	Ser Arg Gln Arg	Ser Arg Asp Pro			
	435	440	445			
Arg Asp Ala Gly	Phe Arg Ser Arg	Asp Pro Gln Tyr	Asp Gly Arg Leu			
	450	455	460			
Leu Glu Glu Ala	Leu Lys Lys Lys	Gly Ser Gly Glu	Arg Arg Arg Val			
465	470	475	480			
Tyr Arg Glu Glu	Glu Glu Glu Glu	Gly Gln Tyr Pro	Pro Ala Pro			
	485	490	495			
Pro Pro Tyr Ser	Glu Thr Asp Ser	Gln Ala Ser Arg	Glu Arg Arg Leu			
	500	505	510			
Lys Lys Asn Leu	Ala Leu Ser Arg	Glu Ser Leu Val	Val			
	515	520	525			

<210> 7
 <211> 2158
 <212> DNA
 <213> Homo sapiens

<220>

<221> Misc_Feature
 <222> 1259..1261
 <223> Potential splicing site AAG

<221> Misc_Feature
 <222> 1657
 <223> Potential insertion of a AGG

<400> 7

tggagtgtgg ctcggaggac cgcggcgggt caagcacctt tctcccccat atctgaaagc	60
atgccctttg tccacgtcgt ttacgctcat taaaacttcc aga atg caa cag gac	115
Met Gln Gln Asp	
1	
gga ctt gga gta ggg aca agg aac gga agt ggg aag ggg agg agc gtg	163
Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys Gly Arg Ser Val	
5 10 15 20	
cac ccc tcc tgg cct tgg tgc gcg ccg cgc ccc cta agg tac ttt gga	211
His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu Arg Tyr Phe Gly	
25 30 35	
agg gac gcg cgg gcc aga cgc gcc cag acg gcc gcg atg gcg ctg ttg	259
Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala Met Ala Leu Leu	
40 45 50	
gcc ggc ggg ctc tcc aga ggg ctg ggc tcc cac ccg gcc gcc gca ggc	307
Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro Ala Ala Ala Gly	
55 60 65	
cgg gac gcg gtc gtc ttc gtg tgg ctt ctg ctt agc acc tgg tgc aca	355
Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser Thr Trp Cys Thr	
70 75 80	
gct cct gcc agg gcc atc cag gtg acc gtg tcc aac ccc tac cac gtg	403
Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn Pro Tyr His Val	
85 90 95 100	
gtg atc ctc ttc cag cct gtg acc ctg ccc tgt acc tac cag atg acc	451
Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Thr	
105 110 115	
tcg acc ccc acg caa ccc atc gtc atc tgg aag tac aag tct ttc tgc	499
Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys	
120 125 130	

cgg gac cgc atc gcc gat gcc ttc tcc ccg gcc agc gtc gac aac cag	547
Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln	
135 140 145	
ctc aat gcc cag ctg gca gcc ggg aac cca ggc tac aac ccc tac gtt	595
Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val	
150 155 160	
gag tgc cag gac agc gtg cgc acc gtc agg gtc gtg gcc acc aag cag	643
Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln	
165 170 175 180	
ggc aac gct gtg acc ctg gga gat tac tac cag ggc cgg agg att acc	691
Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr	
185 190 195	
atc acc gga aat gct gac ctg acc ttt gac cag acg gcg tgg ggg gac	739
Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr Ala Trp Gly Asp	
200 205 210	
agt ggt gtg tat tac tgc tcc gtg gtc tca gcc cag gac ctc cag ggg	787
Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Gln Gly	
215 220 225	
aac aat gag gcc tac gca gag ctc atc gtc ctt ggg agg acc tca ggg	835
Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Gly Arg Thr Ser Gly	
230 235 240	
gtg gct gag ctc tta cct ggt ttt cag gcg ggg ccc ata gaa gac tgg	883
Val Ala Glu Leu Leu Pro Gly Phe Gln Ala Gly Pro Ile Glu Asp Trp	
245 250 255 260	
ctc ttc gtg gtt gtg gta tgc ctg gct gcc ttc ctc atc ttc ctc ctc	931
Leu Phe Val Val Val Val Cys Leu Ala Ala Phe Leu Ile Phe Leu Leu	
265 270 275	
ctg ggc atc tgc tgg tgc cag tgc tgc ccg cac act tgc tgc tgc tac	979
Leu Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr Cys Cys Cys Tyr	
280 285 290	
gtc agg tgc ccc tgc tgc cca gac aag tgc tgc tgc ccc gag gcc ctg	1027
Val Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Cys Pro Glu Ala Leu	
295 300 305	
tat gcc gcc ggc aaa gca gcc acc tca ggt gtt ccc agc att tat gcc	1075
Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala	
310 315 320	
ccc agc acc tat gcc cac ctg tct ccc gcc aag acc cca ccc cca cca	1123
Pro Ser Thr Tyr Ala His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro	
325 330 335 340	
gct atg att ccc atg ggc cct gcc tac aac ggg tac cct gga gga tac	1171
Ala Met Ile Pro Met Gly Pro Ala Tyr Asn Gly Tyr Pro Gly Gly Tyr	
345 350 355	
cct gga gac gtt gac agg agt agc tca gct ggt ggc caa ggc tcc tat	1219

Pro	Gly	Asp	Val	Asp	Arg	Ser	Ser	Ser	Ala	Gly	Gly	Gln	Gly	Ser	Tyr	
			360					365					370			
gta	ccc	ctg	ctt	cgg	gac	acg	gac	agc	agt	gtg	gcc	tct	gaa	gtc	cgc	1267
Val	Pro	Leu	Leu	Arg	Asp	Thr	Asp	Ser	Ser	Val	Ala	Ser	Glu	Val	Arg	
		375					380					385				
agt	ggc	tac	agg	att	cag	gcc	agc	cag	cag	gac	gac	tcc	atg	cgg	gtc	1315
Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Ser	Gln	Gln	Asp	Asp	Ser	Met	Arg	Val	
	390					395					400					
ctg	tac	tac	atg	gag	aag	gag	ctg	gcc	aac	ttc	gac	cct	tct	cga	cct	1363
Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser	Arg	Pro	
405					410					415					420	
ggc	ccc	ccc	agt	ggc	cgt	gtg	gag	cgg	gcc	atg	agt	gaa	gtc	acc	tcc	1411
Gly	Pro	Pro	Ser	Gly	Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val	Thr	Ser	
				425					430					435		
ctc	cac	gag	gac	gac	tgg	cga	tct	cgg	cct	tcc	cgg	ggc	cct	gcc	ctc	1459
Leu	His	Glu	Asp	Asp	Trp	Arg	Ser	Arg	Pro	Ser	Arg	Gly	Pro	Ala	Leu	
			440					445					450			
acc	ccg	atc	cgg	gat	gag	gag	tgg	ggc	ggc	cac	tcc	ccc	cgg	agt	ccc	1507
Thr	Pro	Ile	Arg	Asp	Glu	Glu	Trp	Gly	Gly	His	Ser	Pro	Arg	Ser	Pro	
		455					460					465				
agg	gga	tgg	gac	cag	gag	ccc	gcc	agg	gag	cag	gca	ggc	ggg	ggc	tgg	1555
Arg	Gly	Trp	Asp	Gln	Glu	Pro	Ala	Arg	Glu	Gln	Ala	Gly	Gly	Gly	Trp	
	470					475					480					
cgg	gcc	agg	cgg	ccc	cgg	gcc	cgc	tcc	gtg	gac	gcc	ctg	gac	gac	ctc	1603
Arg	Ala	Arg	Arg	Pro	Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp	Asp	Leu	
485					490					495					500	
acc	ccg	ccg	agc	acc	gcc	gag	tca	ggg	agc	agg	tct	ccc	acg	agt	aat	1651
Thr	Pro	Pro	Ser	Thr	Ala	Glu	Ser	Gly	Ser	Arg	Ser	Pro	Thr	Ser	Asn	
				505					510					515		
ggc	ggg	aga	agc	cgg	gcc	tac	atg	ccc	ccg	cgg	agc	cgc	agc	cgg	gac	1699
Gly	Gly	Arg	Ser	Arg	Ala	Tyr	Met	Pro	Pro	Arg	Ser	Arg	Ser	Arg	Asp	
			520					525					530			
gac	ctc	tat	gac	caa	gac	gac	tcg	agg	gac	ttc	cca	cgc	tcc	cgg	gac	1747
Asp	Leu	Tyr	Asp	Gln	Asp	Asp	Ser	Arg	Asp	Phe	Pro	Arg	Ser	Arg	Asp	
		535					540					545				
ccc	cac	tac	gac	gac	ttc	agg	tct	cgg	gag	cgc	cct	cct	gcc	gac	ccc	1795
Pro	His	Tyr	Asp	Asp	Phe	Arg	Ser	Arg	Glu	Arg	Pro	Pro	Ala	Asp	Pro	
	550					555					560					
agg	tcc	cac	cac	cac	cgt	acc	cgg	gac	cct	cgg	gac	aac	ggc	tcc	agg	1843
Arg	Ser	His	His	His	Arg	Thr	Arg	Asp	Pro	Arg	Asp	Asn	Gly	Ser	Arg	
565					570					575					580	

tcc ggg gac ctc ccc tat gat ggg cgg cta ctg gag gag gct gtg agg Ser Gly Asp Leu Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val Arg 585 590 595	1891
aag aag ggg tcg gag gag agg agg aga ccc cac aag gag gag gag gaa Lys Lys Gly Ser Glu Glu Arg Arg Arg Pro His Lys Glu Glu Glu Glu 600 605 610	1939
gag gcc tac tac ccg ccc gcg ccg ccc ccg tac tcg gag acc gac tcg Glu Ala Tyr Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser 615 620 625	1987
cag gcg tcc cga gag cgc agg ctc aag aag aac ttg gcc ctg agt cgg Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg 630 635 640	2035
gaa agt tta gtc gtc tga tctgacgttt tctacgtagc ttttgtatatt Glu Ser Leu Val Val * 645	2083
tttttttttaa tttgaaggaa cactgatgaa gccctgccat acccctcccg agtctaataa	2143
aacgtataat cacaa	2158
<210> 8	
<211> 649	
<212> PRT	
<213> Homo sapiens	
<220>	
<221> Misc_Feature	
<222> 386	
<223> Potential deletion of a Glu	
<221> Misc_Feature	
<222> 518	
<223> Potential insertion of a Arg	
<400> 8	
Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys 1 5 10 15	
Gly Arg Ser Val His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu 20 25 30	
Arg Tyr Phe Gly Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala 35 40 45	
Met Ala Leu Leu Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro 50 55 60	
Ala Ala Ala Gly Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser 65 70 75 80	

Thr Trp Cys Thr Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn
 85 90 95
 Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr
 100 105 110
 Tyr Gln Met Thr Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr
 115 120 125
 Lys Ser Phe Cys Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser
 130 135 140
 Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr
 145 150 155 160
 Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val
 165 170 175
 Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly
 180 185 190
 Arg Arg Ile Thr Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr
 195 200 205
 Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln
 210 215 220
 Asp Leu Gln Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Gly
 225 230 235 240
 Arg Thr Ser Gly Val Ala Glu Leu Leu Pro Gly Phe Gln Ala Gly Pro
 245 250 255
 Ile Glu Asp Trp Leu Phe Val Val Val Val Cys Leu Ala Ala Phe Leu
 260 265 270
 Ile Phe Leu Leu Leu Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr
 275 280 285
 Cys Cys Cys Tyr Val Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Cys
 290 295 300
 Pro Glu Ala Leu Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro
 305 310 315 320
 Ser Ile Tyr Ala Pro Ser Thr Tyr Ala His Leu Ser Pro Ala Lys Thr
 325 330 335
 Pro Pro Pro Pro Ala Met Ile Pro Met Gly Pro Ala Tyr Asn Gly Tyr
 340 345 350
 Pro Gly Gly Tyr Pro Gly Asp Val Asp Arg Ser Ser Ser Ala Gly Gly
 355 360 365
 Gln Gly Ser Tyr Val Pro Leu Leu Arg Asp Thr Asp Ser Ser Val Ala
 370 375 380

Ser Glu Val Arg Ser Gly Tyr Arg Ile Gln Ala Ser Gln Gln Asp Asp
 385 390 395 400
 Ser Met Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp
 405 410 415
 Pro Ser Arg Pro Gly Pro Pro Ser Gly Arg Val Glu Arg Ala Met Ser
 420 425 430
 Glu Val Thr Ser Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg
 435 440 445
 Gly Pro Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp Gly Gly His Ser
 450 455 460
 Pro Arg Ser Pro Arg Gly Trp Asp Gln Glu Pro Ala Arg Glu Gln Ala
 465 470 475 480
 Gly Gly Gly Trp Arg Ala Arg Arg Pro Arg Ala Arg Ser Val Asp Ala
 485 490 495
 Leu Asp Asp Leu Thr Pro Pro Ser Thr Ala Glu Ser Gly Ser Arg Ser
 500 505 510
 Pro Thr Ser Asn Gly Gly Arg Ser Arg Ala Tyr Met Pro Pro Arg Ser
 515 520 525
 Arg Ser Arg Asp Asp Leu Tyr Asp Gln Asp Asp Ser Arg Asp Phe Pro
 530 535 540
 Arg Ser Arg Asp Pro His Tyr Asp Asp Phe Arg Ser Arg Glu Arg Pro
 545 550 555 560
 Pro Ala Asp Pro Arg Ser His His His Arg Thr Arg Asp Pro Arg Asp
 565 570 575
 Asn Gly Ser Arg Ser Gly Asp Leu Pro Tyr Asp Gly Arg Leu Leu Glu
 580 585 590
 Glu Ala Val Arg Lys Lys Gly Ser Glu Glu Arg Arg Arg Pro His Lys
 595 600 605
 Glu Glu Glu Glu Glu Ala Tyr Tyr Pro Pro Ala Pro Pro Pro Tyr Ser
 610 615 620
 Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu
 625 630 635 640
 Ala Leu Ser Arg Glu Ser Leu Val Val
 645

<210> 9
 <211> 2101
 <212> DNA
 <213> Homo sapiens

<400> 9

tggagtgtgg ctcggaggac cgcggcgggt caagcacctt tctcccccat atctgaaagc	60
atgccctttg tccacgtcgt ttacgctcat taaaacttcc aga atg caa cag gac	115
Met Gln Gln Asp	
1	
gga ctt gga gta ggg aca agg aac gga agt ggg aag ggg agg agc gtg	163
Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys Gly Arg Ser Val	
5 10 15 20	
cac ccc tcc tgg cct tgg tgc gcg ccg cgc ccc cta agg tac ttt gga	211
His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu Arg Tyr Phe Gly	
25 30 35	
agg gac gcg cgg gcc aga cgc gcc cag acg gcc gcg atg gcg ctg ttg	259
Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala Met Ala Leu Leu	
40 45 50	
gcc ggc ggg ctc tcc aga ggg ctg ggc tcc cac ccg gcc gcc gca ggc	307
Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro Ala Ala Ala Gly	
55 60 65	
cgg gac gcg gtc gtc ttc gtg tgg ctt ctg ctt agc acc tgg tgc aca	355
Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser Thr Trp Cys Thr	
70 75 80	
gct cct gcc agg gcc atc cag gtg acc gtg tcc aac ccc tac cac gtg	403
Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn Pro Tyr His Val	
85 90 95 100	
gtg atc ctc ttc cag cct gtg acc ctg ccc tgt acc tac cag atg acc	451
Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Thr	
105 110 115	
tcg acc ccc acg caa ccc atc gtc atc tgg aag tac aag tct ttc tgc	499
Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys	
120 125 130	
cgg gac cgc atc gcc gat gcc ttc tcc ccg gcc agc gtc gac aac cag	547
Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln	
135 140 145	
ctc aat gcc cag ctg gca gcc ggg aac cca ggc tac aac ccc tac gtt	595
Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val	
150 155 160	
gag tgc cag gac agc gtg cgc acc gtc agg gtc gtg gcc acc aag cag	643
Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln	
165 170 175 180	
ggc aac gct gtg acc ctg gga gat tac tac cag ggc cgg agg att acc	691
Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr	
185 190 195	
atc acc gga aat gct gac ctg acc ttt gac cag acg gcg tgg ggg gac	739

Ile	Thr	Gly	Asn	Ala	Asp	Leu	Thr	Phe	Asp	Gln	Thr	Ala	Trp	Gly	Asp		
			200					205					210				
agt	ggt	gtg	tat	tac	tgc	tcc	gtg	gtc	tca	gcc	cag	gac	ctc	cag	ggg	787	
Ser	Gly	Val	Tyr	Tyr	Cys	Ser	Val	Val	Ser	Ala	Gln	Asp	Leu	Gln	Gly		
		215					220					225					
aac	aat	gag	gcc	tac	gca	gag	ctc	atc	gtc	ctt	gac	tgg	ctc	ttc	gtg	835	
Asn	Asn	Glu	Ala	Tyr	Ala	Glu	Leu	Ile	Val	Leu	Asp	Trp	Leu	Phe	Val		
	230					235					240						
gtt	gtg	gta	tgc	ctg	gct	gcc	ttc	ctc	atc	ttc	ctc	ctc	ctg	ggc	atc	883	
Val	Val	Val	Cys	Leu	Ala	Ala	Phe	Leu	Ile	Phe	Leu	Leu	Leu	Gly	Ile		
245					250					255					260		
tgc	tgg	tgc	cag	tgc	tgc	ccg	cac	act	tgc	tgc	tgc	tac	gtc	agg	tgc	931	
Cys	Trp	Cys	Gln	Cys	Cys	Pro	His	Thr	Cys	Cys	Cys	Tyr	Val	Arg	Cys		
				265					270					275			
ccc	tgc	tgc	cca	gac	aag	tgc	tgc	tgc	ccc	gag	gcc	ctg	tat	gcc	gcc	979	
Pro	Cys	Cys	Pro	Asp	Lys	Cys	Cys	Cys	Pro	Glu	Ala	Leu	Tyr	Ala	Ala		
			280					285					290				
ggc	aaa	gca	gcc	acc	tca	ggt	gtt	ccc	agc	att	tat	gcc	ccc	agc	acc	1027	
Gly	Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Thr		
		295					300					305					
tat	gcc	cac	ctg	tct	ccc	gcc	aag	acc	cca	ccc	cca	cca	gct	atg	att	1075	
Tyr	Ala	His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro	Pro	Ala	Met	Ile		
	310					315					320						
ccc	atg	ggc	cct	gcc	tac	aac	ggg	tac	cct	gga	gga	tac	cct	gga	gac	1123	
Pro	Met	Gly	Pro	Ala	Tyr	Asn	Gly	Tyr	Pro	Gly	Gly	Tyr	Pro	Gly	Asp		
325					330				335						340		
gtt	gac	agg	agt	agc	tca	gct	ggt	ggc	caa	ggc	tcc	tat	gta	ccc	ctg	1171	
Val	Asp	Arg	Ser	Ser	Ser	Ala	Gly	Gly	Gln	Gly	Ser	Tyr	Val	Pro	Leu		
				345					350					355			
ctt	cgg	gac	acg	gac	agc	agt	gtg	gcc	tct	gaa	gtc	cgc	agt	ggc	tac	1219	
Leu	Arg	Asp	Thr	Asp	Ser	Ser	Val	Ala	Ser	Glu	Val	Arg	Ser	Gly	Tyr		
			360					365					370				
agg	att	cag	gcc	agc	cag	cag	gac	gac	tcc	atg	cgg	gtc	ctg	tac	tac	1267	
Arg	Ile	Gln	Ala	Ser	Gln	Gln	Asp	Asp	Ser	Met	Arg	Val	Leu	Tyr	Tyr		
		375					380					385					
atg	gag	aag	gag	ctg	gcc	aac	ttc	gac	cct	tct	cga	cct	ggc	ccc	ccc	1315	
Met	Glu	Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser	Arg	Pro	Gly	Pro	Pro		
	390					395					400						
agt	ggc	cgt	gtg	gag	cgg	gcc	atg	agt	gaa	gtc	acc	tcc	ctc	cac	gag	1363	
Ser	Gly	Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val	Thr	Ser	Leu	His	Glu		
405					410					415					420		

gac gac tgg cga tct cgg cct tcc cgg ggc cct gcc ctc acc ccg atc Asp Asp Trp Arg Ser Arg Pro Ser Arg Gly Pro Ala Leu Thr Pro Ile 425 430 435	1411
cgg gat gag gag tgg ggt ggc cac tcc ccc cgg agt ccc agg gga tgg Arg Asp Glu Glu Trp Gly Gly His Ser Pro Arg Ser Pro Arg Gly Trp 440 445 450	1459
gac cag gag ccc gcc agg gag cag gca ggc ggg ggc tgg cgg gcc agg Asp Gln Glu Pro Ala Arg Glu Gln Ala Gly Gly Gly Trp Arg Ala Arg 455 460 465	1507
cgg ccc cgg gcc cgc tcc gtg gac gcc ctg gac gac ctc acc ccg ccg Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Leu Thr Pro Pro 470 475 480	1555
agc acc gcc gag tca ggg agc agg tct ccc acg agt aat ggt ggg aga Ser Thr Ala Glu Ser Gly Ser Arg Ser Pro Thr Ser Asn Gly Gly Arg 485 490 495 500	1603
agc cgg gcc tac atg ccc ccg cgg agc cgc agc cgg gac gac ctc tat Ser Arg Ala Tyr Met Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr 505 510 515	1651
gac caa gac gac tcg agg gac ttc cca cgc tcc cgg gac ccc cac tac Asp Gln Asp Asp Ser Arg Asp Phe Pro Arg Ser Arg Asp Pro His Tyr 520 525 530	1699
gac gac ttc agg tct cgg gag cgc cct cct gcc gac ccc agg tcc cac Asp Asp Phe Arg Ser Arg Glu Arg Pro Pro Ala Asp Pro Arg Ser His 535 540 545	1747
cac cac cgt acc cgg gac cct cgg gac aac ggc tcc agg tcc ggg gac His His Arg Thr Arg Asp Pro Arg Asp Asn Gly Ser Arg Ser Gly Asp 550 555 560	1795
ctc ccc tat gat ggg cgg cta ctg gag gag gct gtg agg aag aag ggg Leu Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val Arg Lys Lys Gly 565 570 575 580	1843
tcg gag gag agg agg aga ccc cac aag gag gag gag gaa gag gcc tac Ser Glu Glu Arg Arg Arg Pro His Lys Glu Glu Glu Glu Glu Ala Tyr 585 590 595	1891
tac ccg ccc gcg ccg ccc ccg tac tcg gag acc gac tcg cag gcg tcc Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser 600 605 610	1939
cga gag cgc agg ctc aag aag aac ttg gcc ctg agt cgg gaa agt tta Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu 615 620 625	1987
gtc gtc tga tctgacgttt tctacgtagc ttttgtattt ttttttttaa Val Val * 630	2036
tttgaaggaa cactgatgaa gccctgccat acccctcccg agtctaataa aacgtataat	2096

cacaa

2101

<210> 10
<211> 630
<212> PRT
<213> Homo sapiens

<400> 10
Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys
1 5 10 15
Gly Arg Ser Val His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu
20 25 30
Arg Tyr Phe Gly Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala
35 40 45
Met Ala Leu Leu Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro
50 55 60
Ala Ala Ala Gly Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser
65 70 75 80
Thr Trp Cys Thr Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn
85 90 95
Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr
100 105 110
Tyr Gln Met Thr Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr
115 120 125
Lys Ser Phe Cys Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser
130 135 140
Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr
145 150 155 160
Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val
165 170 175
Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly
180 185 190
Arg Arg Ile Thr Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr
195 200 205
Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln
210 215 220
Asp Leu Gln Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Asp
225 230 235 240
Trp Leu Phe Val Val Val Val Cys Leu Ala Ala Phe Leu Ile Phe Leu

245								250				255			
Leu	Leu	Gly	Ile	Cys	Trp	Cys	Gln	Cys	Cys	Pro	His	Thr	Cys	Cys	Cys
			260						265					270	
Tyr	Val	Arg	Cys	Pro	Cys	Cys	Pro	Asp	Lys	Cys	Cys	Cys	Pro	Glu	Ala
		275					280					285			
Leu	Tyr	Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr
	290					295					300				
Ala	Pro	Ser	Thr	Tyr	Ala	His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro
305					310					315					320
Pro	Ala	Met	Ile	Pro	Met	Gly	Pro	Ala	Tyr	Asn	Gly	Tyr	Pro	Gly	Gly
				325					330					335	
Tyr	Pro	Gly	Asp	Val	Asp	Arg	Ser	Ser	Ser	Ala	Gly	Gly	Gln	Gly	Ser
			340						345					350	
Tyr	Val	Pro	Leu	Leu	Arg	Asp	Thr	Asp	Ser	Ser	Val	Ala	Ser	Glu	Val
		355					360					365			
Arg	Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Ser	Gln	Gln	Asp	Asp	Ser	Met	Arg
	370					375					380				
Val	Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser	Arg
385					390					395					400
Pro	Gly	Pro	Pro	Ser	Gly	Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val	Thr
				405					410					415	
Ser	Leu	His	Glu	Asp	Asp	Trp	Arg	Ser	Arg	Pro	Ser	Arg	Gly	Pro	Ala
			420						425					430	
Leu	Thr	Pro	Ile	Arg	Asp	Glu	Glu	Trp	Gly	Gly	His	Ser	Pro	Arg	Ser
		435					440					445			
Pro	Arg	Gly	Trp	Asp	Gln	Glu	Pro	Ala	Arg	Glu	Gln	Ala	Gly	Gly	Gly
	450					455					460				
Trp	Arg	Ala	Arg	Arg	Pro	Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp	Asp
465					470					475					480
Leu	Thr	Pro	Pro	Ser	Thr	Ala	Glu	Ser	Gly	Ser	Arg	Ser	Pro	Thr	Ser
				485					490					495	
Asn	Gly	Gly	Arg	Ser	Arg	Ala	Tyr	Met	Pro	Pro	Arg	Ser	Arg	Ser	Arg
			500						505					510	
Asp	Asp	Leu	Tyr	Asp	Gln	Asp	Asp	Ser	Arg	Asp	Phe	Pro	Arg	Ser	Arg
		515					520					525			
Asp	Pro	His	Tyr	Asp	Asp	Phe	Arg	Ser	Arg	Glu	Arg	Pro	Pro	Ala	Asp
	530					535					540				
Pro	Arg	Ser	His	His	His	Arg	Thr	Arg	Asp	Pro	Arg	Asp	Asn	Gly	Ser

545		550		555		560
Arg Ser Gly Asp Leu Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val						
		565		570		575
Arg Lys Lys Gly Ser Glu Glu Arg Arg Arg Pro His Lys Glu Glu Glu						
		580		585		590
Glu Glu Ala Tyr Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp						
		595		600		605
Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser						
		610		615		620
Arg Glu Ser Leu Val Val						
625		630				

<210> 11
 <211> 1954
 <212> DNA
 <213> Homo sapiens

<400> 11	
tggagtgtgg ctcggaggac cgcggcgggt caagcacctt tctcccccat atctgaaagc	60
atgccctttg tccacgtcgt ttacgtctcat taaaacttcc aga atg caa cag gac	115
	Met Gln Gln Asp
	1
gga ctt gga gta ggg aca agg aac gga agt ggg aag ggg agg agc gtg	163
Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys Gly Arg Ser Val	
5	10 15 20
cac ccc tcc tgg cct tgg tgc gcg ccg cgc ccc cta agg tac ttt gga	211
His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu Arg Tyr Phe Gly	
	25 30 35
agg gac gcg cgg gcc aga cgc gcc cag acg gcc gcg atg gcg ctg ttg	259
Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala Met Ala Leu Leu	
	40 45 50
gcc ggc ggg ctc tcc aga ggg ctg ggc tcc cac ccg gcc gcc gca ggc	307
Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro Ala Ala Ala Gly	
	55 60 65
cgg gac gcg gtc gtc ttc gtg tgg ctt ctg ctt agc acc tgg tgc aca	355
Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser Thr Trp Cys Thr	
	70 75 80
gct cct gcc agg gcc atc cag gtg acc gtg tcc aac ccc tac cac gtg	403
Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn Pro Tyr His Val	
85	90 95 100
gtg atc ctc ttc cag cct gtg acc ctg ccc tgt acc tac cag atg acc	451

Val	Ile	Leu	Phe	Gln	Pro	Val	Thr	Leu	Pro	Cys	Thr	Tyr	Gln	Met	Thr		
				105					110					115			
tcg	acc	ccc	acg	caa	ccc	atc	gtc	atc	tgg	aag	tac	aag	tct	ttc	tgc		499
Ser	Thr	Pro	Thr	Gln	Pro	Ile	Val	Ile	Trp	Lys	Tyr	Lys	Ser	Phe	Cys		
			120				125						130				
cgg	gac	cgc	atc	gcc	gat	gcc	ttc	tcc	ccg	gcc	agc	gtc	gac	aac	cag		547
Arg	Asp	Arg	Ile	Ala	Asp	Ala	Phe	Ser	Pro	Ala	Ser	Val	Asp	Asn	Gln		
		135					140					145					
ctc	aat	gcc	cag	ctg	gca	gcc	ggg	aac	cca	ggc	tac	aac	ccc	tac	gtt		595
Leu	Asn	Ala	Gln	Leu	Ala	Ala	Gly	Asn	Pro	Gly	Tyr	Asn	Pro	Tyr	Val		
	150					155					160						
gag	tgc	cag	gac	agc	gtg	cgc	acc	gtc	agg	gtc	gtg	gcc	acc	aag	cag		643
Glu	Cys	Gln	Asp	Ser	Val	Arg	Thr	Val	Arg	Val	Val	Ala	Thr	Lys	Gln		
165					170				175						180		
ggc	aac	gct	gtg	acc	ctg	gga	gat	tac	tac	cag	ggc	cgg	agg	att	acc		691
Gly	Asn	Ala	Val	Thr	Leu	Gly	Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr		
				185					190					195			
atc	acc	gga	aat	gct	gac	ctg	acc	ttt	gac	cag	acg	gcg	tgg	ggg	gac		739
Ile	Thr	Gly	Asn	Ala	Asp	Leu	Thr	Phe	Asp	Gln	Thr	Ala	Trp	Gly	Asp		
			200					205					210				
agt	ggt	gtg	tat	tac	tgc	tcc	gtg	gtc	tca	gcc	cag	gac	ctc	cag	ggg		787
Ser	Gly	Val	Tyr	Tyr	Cys	Ser	Val	Val	Ser	Ala	Gln	Asp	Leu	Gln	Gly		
		215					220					225					
aac	aat	gag	gcc	tac	gca	gag	ctc	atc	gtc	ctt	gtg	tat	gcc	gcc	ggc		835
Asn	Asn	Glu	Ala	Tyr	Ala	Glu	Leu	Ile	Val	Leu	Val	Tyr	Ala	Ala	Gly		
	230					235					240						
aaa	gca	gcc	acc	tca	ggt	gtt	ccc	agc	att	tat	gcc	ccc	agc	acc	tat		883
Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Thr	Tyr		
245					250				255						260		
gcc	cac	ctg	tct	ccc	gcc	aag	acc	cca	ccc	cca	cca	gct	atg	att	ccc		931
Ala	His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro	Pro	Ala	Met	Ile	Pro		
				265				270						275			
atg	ggc	cct	gcc	tac	aac	ggg	tac	cct	gga	gga	tac	cct	gga	gac	gtt		979
Met	Gly	Pro	Ala	Tyr	Asn	Gly	Tyr	Pro	Gly	Gly	Tyr	Pro	Gly	Asp	Val		
			280					285					290				
gac	agg	agt	agc	tca	gct	ggt	ggc	caa	ggc	tcc	tat	gta	ccc	ctg	ctt		1027
Asp	Arg	Ser	Ser	Ser	Ala	Gly	Gly	Gln	Gly	Ser	Tyr	Val	Pro	Leu	Leu		
		295					300					305					
cgg	gac	acg	gac	agc	agt	gtg	gcc	tct	gaa	gtc	cgc	agt	ggc	tac	agg		1075
Arg	Asp	Thr	Asp	Ser	Ser	Val	Ala	Ser	Glu	Val	Arg	Ser	Gly	Tyr	Arg		
	310					315					320						
att	cag	gcc	agc	cag	cag	gac	gac	tcc	atg	cgg	gtc	ctg	tac	tac	atg		1123
Ile	Gln	Ala	Ser	Gln	Gln	Asp	Asp	Ser	Met	Arg	Val	Leu	Tyr	Tyr	Met		

325		330		335		340	
gag aag gag ctg gcc aac ttc gac cct tct cga cct ggc ccc ccc agt							1171
Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro Pro Ser							
		345		350		355	
ggc cgt gtg gag cgg gcc atg agt gaa gtc acc tcc ctc cac gag gac							1219
Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser Leu His Glu Asp							
		360		365		370	
gac tgg cga tct cgg cct tcc cgg ggc cct gcc ctc acc ccg atc cgg							1267
Asp Trp Arg Ser Arg Pro Ser Arg Gly Pro Ala Leu Thr Pro Ile Arg							
		375		380		385	
gat gag gag tgg ggt ggc cac tcc ccc cgg agt ccc agg gga tgg gac							1315
Asp Glu Glu Trp Gly Gly His Ser Pro Arg Ser Pro Arg Gly Trp Asp							
		390		395		400	
cag gag ccc gcc agg gag cag gca ggc ggg ggc tgg cgg gcc agg cgg							1363
Gln Glu Pro Ala Arg Glu Gln Ala Gly Gly Gly Trp Arg Ala Arg Arg							
		405		410		415	420
ccc cgg gcc cgc tcc gtg gac gcc ctg gac gac ctc acc ccg ccg agc							1411
Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Leu Thr Pro Pro Ser							
		425		430		435	
acc gcc gag tca ggg agc agg tct ccc acg agt aat ggt ggg aga agc							1459
Thr Ala Glu Ser Gly Ser Arg Ser Pro Thr Ser Asn Gly Gly Arg Ser							
		440		445		450	
cgg gcc tac atg ccc ccg cgg agc cgc agc cgg gac gac ctc tat gac							1507
Arg Ala Tyr Met Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp							
		455		460		465	
caa gac gac tcg agg gac ttc cca cgc tcc cgg gac ccc cac tac gac							1555
Gln Asp Asp Ser Arg Asp Phe Pro Arg Ser Arg Asp Pro His Tyr Asp							
		470		475		480	
gac ttc agg tct cgg gag cgc cct cct gcc gac ccc agg tcc cac cac							1603
Asp Phe Arg Ser Arg Glu Arg Pro Pro Ala Asp Pro Arg Ser His His							
		485		490		495	500
cac cgt acc cgg gac cct cgg gac aac ggc tcc agg tcc ggg gac ctc							1651
His Arg Thr Arg Asp Pro Arg Asp Asn Gly Ser Arg Ser Gly Asp Leu							
		505		510		515	
ccc tat gat ggg cgg cta ctg gag gag gct gtg agg aag aag ggg tcg							1699
Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val Arg Lys Lys Gly Ser							
		520		525		530	
gag gag agg agg aga ccc cac aag gag gag gag gaa gag gcc tac tac							1747
Glu Glu Arg Arg Arg Pro His Lys Glu Glu Glu Glu Glu Ala Tyr Tyr							
		535		540		545	
ccg ccc gcg ccg ccc ccg tac tcg gag acc gac tcg cag gcg tcc cga							1795
Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg							
		550		555		560	

gag cgc agg ctc aag aag aac ttg gcc ctg agt cgg gaa agt tta gtc 1843
 Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val
 565 570 575 580

gtc tga tctgacgttt tctacgtagc ttttgtattt ttttttttaa tttgaaggaa 1899
 Val *

cactgatgaa gccctgccat acccctcccg agtctaataa aacgtataat cacaa 1954

<210> 12
 <211> 581
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys
 1 5 10 15
 Gly Arg Ser Val His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu
 20 25 30
 Arg Tyr Phe Gly Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala
 35 40 45
 Met Ala Leu Leu Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro
 50 55 60
 Ala Ala Ala Gly Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser
 65 70 75 80
 Thr Trp Cys Thr Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn
 85 90 95
 Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr
 100 105 110
 Tyr Gln Met Thr Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr
 115 120 125
 Lys Ser Phe Cys Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser
 130 135 140
 Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr
 145 150 155 160
 Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val
 165 170 175
 Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly
 180 185 190
 Arg Arg Ile Thr Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr
 195 200 205

Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln
 210 215 220
 Asp Leu Gln Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Val
 225 230 235 240
 Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala
 245 250 255
 Pro Ser Thr Tyr Ala His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro
 260 265 270
 Ala Met Ile Pro Met Gly Pro Ala Tyr Asn Gly Tyr Pro Gly Gly Tyr
 275 280 285
 Pro Gly Asp Val Asp Arg Ser Ser Ser Ala Gly Gly Gln Gly Ser Tyr
 290 295 300
 Val Pro Leu Leu Arg Asp Thr Asp Ser Ser Val Ala Ser Glu Val Arg
 305 310 315 320
 Ser Gly Tyr Arg Ile Gln Ala Ser Gln Gln Asp Asp Ser Met Arg Val
 325 330 335
 Leu Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro
 340 345 350
 Gly Pro Pro Ser Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser
 355 360 365
 Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Gly Pro Ala Leu
 370 375 380
 Thr Pro Ile Arg Asp Glu Glu Trp Gly Gly His Ser Pro Arg Ser Pro
 385 390 395 400
 Arg Gly Trp Asp Gln Glu Pro Ala Arg Glu Gln Ala Gly Gly Gly Trp
 405 410 415
 Arg Ala Arg Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Leu
 420 425 430
 Thr Pro Pro Ser Thr Ala Glu Ser Gly Ser Arg Ser Pro Thr Ser Asn
 435 440 445
 Gly Gly Arg Ser Arg Ala Tyr Met Pro Pro Arg Ser Arg Ser Arg Asp
 450 455 460
 Asp Leu Tyr Asp Gln Asp Asp Ser Arg Asp Phe Pro Arg Ser Arg Asp
 465 470 475 480
 Pro His Tyr Asp Asp Phe Arg Ser Arg Glu Arg Pro Pro Ala Asp Pro
 485 490 495
 Arg Ser His His His Arg Thr Arg Asp Pro Arg Asp Asn Gly Ser Arg
 500 505 510

Ser Gly Asp Leu Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val Arg
515 520 525

Lys Lys Gly Ser Glu Glu Arg Arg Arg Pro His Lys Glu Glu Glu Glu
530 535 540

Glu Ala Tyr Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser
545 550 555 560

Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg
565 570 575

Glu Ser Leu Val Val
580

<210> 13
<211> 1886
<212> DNA
<213> Mus musculus

<400> 13

gcaccgtcgc tgctagacgg ccgcg	atg gcg ccg gcg gcc agc gcg tgt gct	52
	Met Ala Pro Ala Ala Ser Ala Cys Ala	
	1 5	
ggg gcg cct ggc tcc cac ccg gcc acc acg atc ttc gtg tgt ctt ttt		100
Gly Ala Pro Gly Ser His Pro Ala Thr Thr Ile Phe Val Cys Leu Phe		
10 15 20 25		
ctc atc att tac tgc cca gac cgt gcc agt gcc atc cag gtg acc gtg		148
Leu Ile Ile Tyr Cys Pro Asp Arg Ala Ser Ala Ile Gln Val Thr Val		
30 35 40		
cct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg aca cta cac		196
Pro Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu His		
45 50 55		
tgc acc tac cag atg agc aat acc ctc aca gcc cct atc gtg atc tgg		244
Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Ala Pro Ile Val Ile Trp		
60 65 70		
aag tat aag tcg ttc tgt cgg gac cgt gtt gcc gac gcc ttc tcc cct		292
Lys Tyr Lys Ser Phe Cys Arg Asp Arg Val Ala Asp Ala Phe Ser Pro		
75 80 85		
gcc agc gtg gac aac cag ctc aac gcc cag ctg gcg gct ggc aac ccc		340
Ala Ser Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro		
90 95 100 105		
ggc tac aac ccc tat gtg gag tgc cag gac agc gta cgc act gtc agg		388
Gly Tyr Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg		
110 115 120		

gtg	gtg	gcc	acc	aaa	cag	ggc	aat	gct	gtg	acc	ctg	gga	gac	tac	tac	436
Val	Val	Ala	Thr	Lys	Gln	Gly	Asn	Ala	Val	Thr	Leu	Gly	Asp	Tyr	Tyr	
		125						130					135			
cag	ggc	agg	aga	atc	acc	atc	aca	gga	aat	gct	ggc	ctg	acc	ttc	gag	484
Gln	Gly	Arg	Arg	Ile	Thr	Ile	Thr	Gly	Asn	Ala	Gly	Leu	Thr	Phe	Glu	
		140						145				150				
cag	acg	gcc	tgg	gga	gac	agt	gga	gtg	tat	tac	tgc	tcc	gtg	gtc	tca	532
Gln	Thr	Ala	Trp	Gly	Asp	Ser	Gly	Val	Tyr	Tyr	Cys	Ser	Val	Val	Ser	
	155					160					165					
gcc	caa	gat	ctg	gat	ggg	aac	aac	gag	gcg	tac	gca	gag	ctc	att	gtc	580
Ala	Gln	Asp	Leu	Asp	Gly	Asn	Asn	Glu	Ala	Tyr	Ala	Glu	Leu	Ile	Val	
170					175					180					185	
ctt	ggc	agg	acc	tca	gaa	gcc	cct	gag	ctc	cta	cct	ggg	ttt	cgg	gcg	628
Leu	Gly	Arg	Thr	Ser	Glu	Ala	Pro	Glu	Leu	Leu	Pro	Gly	Phe	Arg	Ala	
			190					195						200		
ggg	ccc	ttg	gaa	gat	tgg	ctc	ttt	gtg	gtc	gtg	gtc	tgc	ctg	gca	agc	676
Gly	Pro	Leu	Glu	Asp	Trp	Leu	Phe	Val	Val	Val	Val	Cys	Leu	Ala	Ser	
		205						210					215			
ctc	ctc	ttc	ttc	ctc	ctc	ctg	ggc	atc	tgc	tgg	tgc	cag	tgc	tgt	ccc	724
Leu	Leu	Phe	Phe	Leu	Leu	Leu	Gly	Ile	Cys	Trp	Cys	Gln	Cys	Cys	Pro	
		220					225					230				
cac	acc	tgc	tgc	tgc	tat	gtc	aga	tgt	ccc	tgc	tgc	cca	gac	aag	tgc	772
His	Thr	Cys	Cys	Cys	Tyr	Val	Arg	Cys	Pro	Cys	Cys	Pro	Asp	Lys	Cys	
	235					240					245					
tgt	tgc	cct	gag	gcc	ctt	tat	gct	gct	ggc	aaa	gca	gcc	acc	tca	ggg	820
Cys	Cys	Pro	Glu	Ala	Leu	Tyr	Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser	Gly	
250					255				260						265	
gtg	cca	agc	atc	tat	gcc	ccc	agc	atc	tat	acc	cac	ctc	tct	cct	gcc	868
Val	Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Ile	Tyr	Thr	His	Leu	Ser	Pro	Ala	
			270					275						280		
aag	act	ccg	cca	cct	ccg	cct	gcc	atg	att	ccc	atg	cgt	cct	ccc	tat	916
Lys	Thr	Pro	Pro	Pro	Pro	Pro	Ala	Met	Ile	Pro	Met	Arg	Pro	Pro	Tyr	
		285						290					295			
ggg	tac	cct	gga	gac	ttt	gac	agg	acc	agc	tca	gtt	ggg	ggc	cac	agc	964
Gly	Tyr	Pro	Gly	Asp	Phe	Asp	Arg	Thr	Ser	Ser	Val	Gly	Gly	His	Ser	
		300					305					310				
tcc	cag	gtg	ccc	ctg	ctg	cgt	gaa	gtg	gat	ggg	agc	gta	tct	tca	gaa	1012
Ser	Gln	Val	Pro	Leu	Leu	Arg	Glu	Val	Asp	Gly	Ser	Val	Ser	Ser	Glu	
	315					320					325					
gta	cga	agt	ggc	tac	agg	atc	cag	gct	aac	cag	caa	gat	gac	tcc	atg	1060
Val	Arg	Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Asn	Gln	Gln	Asp	Asp	Ser	Met	
330					335					340					345	
agg	gtc	cta	tac	tat	atg	gag	aag	gag	cta	gcc	aac	ttc	gat	cct	tcc	1108

Arg	Val	Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser		
				350					355					360			
cgg	cct	ggc	cct	ccc	aat	ggc	cga	gtg	gaa	cgg	gcc	atg	agt	gaa	gta	1156	
Arg	Pro	Gly	Pro	Pro	Asn	Gly	Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val		
			365					370					375				
acc	tcc	ctc	cat	gaa	gat	gac	tgg	cga	tct	cgg	cct	tcc	agg	gct	cct	1204	
Thr	Ser	Leu	His	Glu	Asp	Asp	Trp	Arg	Ser	Arg	Pro	Ser	Arg	Ala	Pro		
		380					385					390					
gcc	ctc	aca	ccc	atc	agg	gat	gag	gag	tgg	aat	cgc	cac	tcc	cct	cgg	1252	
Ala	Leu	Thr	Pro	Ile	Arg	Asp	Glu	Glu	Trp	Asn	Arg	His	Ser	Pro	Arg		
	395					400					405						
agt	ccc	aga	aca	tgg	gag	cag	gaa	ccc	ctt	caa	gaa	cag	cca	agg	ggt	1300	
Ser	Pro	Arg	Thr	Trp	Glu	Gln	Glu	Pro	Leu	Gln	Glu	Gln	Pro	Arg	Gly		
410					415				420						425		
ggt	tgg	ggg	tct	ggg	cgg	cct	cgg	gcc	cgc	tct	gtg	gat	gct	cta	gat	1348	
Gly	Trp	Gly	Ser	Gly	Arg	Pro	Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp		
				430				435						440			
gac	atc	aac	cgg	cct	ggc	tcc	act	gaa	tca	gga	agg	tct	tct	ccc	cca	1396	
Asp	Ile	Asn	Arg	Pro	Gly	Ser	Thr	Glu	Ser	Gly	Arg	Ser	Ser	Pro	Pro		
		445						450					455				
agt	agt	gga	cgg	aga	ggg	cgg	gcc	tat	gca	cct	ccg	aga	agt	cgc	agc	1444	
Ser	Ser	Gly	Arg	Arg	Gly	Arg	Ala	Tyr	Ala	Pro	Pro	Arg	Ser	Arg	Ser		
		460					465					470					
cgg	gat	gac	ctc	tat	gac	ccc	gac	gat	cct	aga	gac	ttg	cca	cat	tcc	1492	
Arg	Asp	Asp	Leu	Tyr	Asp	Pro	Asp	Asp	Pro	Arg	Asp	Leu	Pro	His	Ser		
	475					480					485						
cga	gat	ccc	cac	tat	tat	gat	gat	ttg	agg	tct	agg	gat	cca	cgt	gct	1540	
Arg	Asp	Pro	His	Tyr	Tyr	Asp	Asp	Leu	Arg	Ser	Arg	Asp	Pro	Arg	Ala		
490					495				500						505		
gac	ccc	aga	tcc	cgt	cag	cga	tcc	cac	gat	cct	cgg	gat	gct	ggc	ttc	1588	
Asp	Pro	Arg	Ser	Arg	Gln	Arg	Ser	His	Asp	Pro	Arg	Asp	Ala	Gly	Phe		
				510				515						520			
agg	tca	cgg	gac	cct	cag	tat	gat	ggg	cga	ctc	tta	gaa	gag	gct	tta	1636	
Arg	Ser	Arg	Asp	Pro	Gln	Tyr	Asp	Gly	Arg	Leu	Leu	Glu	Glu	Ala	Leu		
			525					530					535				
aag	aaa	aaa	ggg	gct	ggg	gag	aga	aga	cgc	gtt	tac	agg	gag	gaa	gaa	1684	
Lys	Lys	Lys	Gly	Ala	Gly	Glu	Arg	Arg	Arg	Val	Tyr	Arg	Glu	Glu	Glu		
		540					545					550					
gaa	gaa	gaa	gag	gag	ggc	cac	tat	ccc	cca	gca	cct	ccg	cct	tac	tct	1732	
Glu	Glu	Glu	Glu	Glu	Gly	His	Tyr	Pro	Pro	Ala	Pro	Pro	Pro	Tyr	Ser		
	555					560					565						
gag	act	gac	tcg	cag	gcc	tcg	agg	gag	cgg	agg	atg	aaa	aag	aat	ttg	1780	
Glu	Thr	Asp	Ser	Gln	Ala	Ser	Arg	Glu	Arg	Arg	Met	Lys	Lys	Asn	Leu		

570	575	580	585	
gcc ctg agt cgg gaa agt tta gtc gtc tga tcccacgttt tgttatgtag				1830
Ala Leu Ser Arg Glu Ser Leu Val Val *				
590				
cttttataact tttttaattg gaatattgat gaaactcttc accaagccta ataaaa				1886
<210> 14				
<211> 1829				
<212> DNA				
<213> Mus musculus				
<400> 14				
gcaccgtcgc tgctagacgg ccgcg atg gcg ccg gcg gcc agc gcg tgt gct				52
Met Ala Pro Ala Ala Ser Ala Cys Ala				
1 5				
ggg gcg cct ggc tcc cac ccg gcc acc acg atc ttc gtg tgt ctt ttt				100
Gly Ala Pro Gly Ser His Pro Ala Thr Thr Ile Phe Val Cys Leu Phe				
10 15 20 25				
ctc atc att tac tgc cca gac cgt gcc agt gcc atc cag gtg acc gtg				148
Leu Ile Ile Tyr Cys Pro Asp Arg Ala Ser Ala Ile Gln Val Thr Val				
30 35 40				
cct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg aca cta cac				196
Pro Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu His				
45 50 55				
tgc acc tac cag atg agc aat acc ctc aca gcc cct atc gtg atc tgg				244
Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Ala Pro Ile Val Ile Trp				
60 65 70				
aag tat aag tcg ttc tgt cgg gac cgt gtt gcc gac gcc ttc tcc cct				292
Lys Tyr Lys Ser Phe Cys Arg Asp Arg Val Ala Asp Ala Phe Ser Pro				
75 80 85				
gcc agc gtg gac aac cag ctc aac gcc cag ctg gcg gct ggc aac ccc				340
Ala Ser Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro				
90 95 100 105				
ggc tac aac ccc tat gtg gag tgc cag gac agc gta cgc act gtc agg				388
Gly Tyr Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg				
110 115 120				
gtg gtg gcc acc aaa cag ggc aat gct gtg acc ctg gga gac tac tac				436
Val Val Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr				
125 130 135				
cag ggc agg aga atc acc atc aca gga aat gct ggc ctg acc ttc gag				484
Gln Gly Arg Arg Ile Thr Ile Thr Gly Asn Ala Gly Leu Thr Phe Glu				
140 145 150				

cag acg gcc tgg gga gac agt gga gtg tat tac tgc tcc gtg gtc tca	532
Gln Thr Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser	
155 160 165	
gcc caa gat ctg gat ggg aac aac gag gcg tac gca gag ctc att gtc	580
Ala Gln Asp Leu Asp Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val	
170 175 180 185	
ctt gat tgg ctc ttt gtg gtc gtg gtc tgc ctg gca agc ctc ctc ttc	628
Leu Asp Trp Leu Phe Val Val Val Val Cys Leu Ala Ser Leu Leu Phe	
190 195 200	
ttc ctc ctc ctg ggc atc tgc tgg tgc cag tgc tgt ccc cac acc tgc	676
Phe Leu Leu Leu Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr Cys	
205 210 215	
tgc tgc tat gtc aga tgt ccc tgc tgc cca gac aag tgc tgt tgc cct	724
Cys Cys Tyr Val Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Cys Pro	
220 225 230	
gag gcc ctt tat gct gct ggc aaa gca gcc acc tca ggt gtg cca agc	772
Glu Ala Leu Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser	
235 240 245	
atc tat gcc ccc agc atc tat acc cac ctc tct cct gcc aag act ccg	820
Ile Tyr Ala Pro Ser Ile Tyr Thr His Leu Ser Pro Ala Lys Thr Pro	
250 255 260 265	
cca cct ccg cct gcc atg att ccc atg cgt cct ccc tat ggg tac cct	868
Pro Pro Pro Pro Ala Met Ile Pro Met Arg Pro Pro Tyr Gly Tyr Pro	
270 275 280	
gga gac ttt gac agg acc agc tca gtt ggt ggc cac agc tcc cag gtg	916
Gly Asp Phe Asp Arg Thr Ser Ser Val Gly Gly His Ser Ser Gln Val	
285 290 295	
ccc ctg ctg cgt gaa gtg gat ggg agc gta tct tca gaa gta cga agt	964
Pro Leu Leu Arg Glu Val Asp Gly Ser Val Ser Ser Glu Val Arg Ser	
300 305 310	
ggc tac agg atc cag gct aac cag caa gat gac tcc atg agg gtc cta	1012
Gly Tyr Arg Ile Gln Ala Asn Gln Gln Asp Asp Ser Met Arg Val Leu	
315 320 325	
tac tat atg gag aag gag cta gcc aac ttc gat cct tcc cgg cct ggc	1060
Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly	
330 335 340 345	
cct ccc aat ggc cga gtg gaa cgg gcc atg agt gaa gta acc tcc ctc	1108
Pro Pro Asn Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser Leu	
350 355 360	
cat gaa gat gac tgg cga tct cgg cct tcc agg gct cct gcc ctc aca	1156
His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala Leu Thr	
365 370 375	
ccc atc agg gat gag gag tgg aat cgc cac tcc cct cgg agt ccc aga	1204

Pro	Ile	Arg	Asp	Glu	Glu	Trp	Asn	Arg	His	Ser	Pro	Arg	Ser	Pro	Arg		
		380					385					390					
aca	tgg	gag	cag	gaa	ccc	ctt	caa	gaa	cag	cca	agg	ggg	ggg	tgg	ggg		1252
Thr	Trp	Glu	Gln	Glu	Pro	Leu	Gln	Glu	Gln	Pro	Arg	Gly	Gly	Trp	Gly		
	395					400					405						
tct	ggg	cgg	cct	cgg	gcc	cgc	tct	gtg	gat	gct	cta	gat	gac	atc	aac		1300
Ser	Gly	Arg	Pro	Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp	Asp	Ile	Asn		
410					415					420					425		
cgg	cct	ggc	tcc	act	gaa	tca	gga	agg	tct	tct	ccc	cca	agt	agt	gga		1348
Arg	Pro	Gly	Ser	Thr	Glu	Ser	Gly	Arg	Ser	Ser	Pro	Pro	Ser	Ser	Gly		
				430					435					440			
cgg	aga	ggg	cgg	gcc	tat	gca	cct	ccg	aga	agt	cgc	agc	cgg	gat	gac		1396
Arg	Arg	Gly	Arg	Ala	Tyr	Ala	Pro	Pro	Arg	Ser	Arg	Ser	Arg	Asp	Asp		
			445					450					455				
ctc	tat	gac	ccc	gac	gat	cct	aga	gac	ttg	cca	cat	tcc	cga	gat	ccc		1444
Leu	Tyr	Asp	Pro	Asp	Asp	Pro	Arg	Asp	Leu	Pro	His	Ser	Arg	Asp	Pro		
		460					465					470					
cac	tat	tat	gat	gat	ttg	agg	tct	agg	gat	cca	cgt	gct	gac	ccc	aga		1492
His	Tyr	Tyr	Asp	Asp	Leu	Arg	Ser	Arg	Asp	Pro	Arg	Ala	Asp	Pro	Arg		
	475					480					485						
tcc	cgt	cag	cga	tcc	cac	gat	cct	cgg	gat	gct	ggc	ttc	agg	tca	cgg		1540
Ser	Arg	Gln	Arg	Ser	His	Asp	Pro	Arg	Asp	Ala	Gly	Phe	Arg	Ser	Arg		
490					495					500					505		
gac	cct	cag	tat	gat	ggg	cga	ctc	tta	gaa	gag	gct	tta	aag	aaa	aaa		1588
Asp	Pro	Gln	Tyr	Asp	Gly	Arg	Leu	Leu	Glu	Glu	Ala	Leu	Lys	Lys	Lys		
				510					515					520			
ggg	gct	ggg	gag	aga	aga	cgc	gtt	tac	agg	gag	gaa	gaa	gaa	gaa	gaa		1636
Gly	Ala	Gly	Glu	Arg	Arg	Arg	Val	Tyr	Arg	Glu	Glu	Glu	Glu	Glu	Glu		
			525					530					535				
gag	gag	ggc	cac	tat	ccc	cca	gca	cct	ccg	cct	tac	tct	gag	act	gac		1684
Glu	Glu	Gly	His	Tyr	Pro	Pro	Ala	Pro	Pro	Pro	Tyr	Ser	Glu	Thr	Asp		
		540					545					550					
tcg	cag	gcc	tcg	agg	gag	cgg	agg	atg	aaa	aag	aat	ttg	gcc	ctg	agt		1732
Ser	Gln	Ala	Ser	Arg	Glu	Arg	Arg	Met	Lys	Lys	Asn	Leu	Ala	Leu	Ser		
	555					560					565						
cgg	gaa	agt	tta	gtc	gtc	tga	tcccacgttt	tggtatgtag	cttttataact								1783
Arg	Glu	Ser	Leu	Val	Val	*											
570					575												
tttttaattg	gaatattgat	gaaactcttc	accaagccta	ataaaa													1829

<210> 15
<211> 1682

<212> DNA
 <213> Mus musculus

<400> 15

gcaccgctcgc tgctagacgg ccgcg atg gcg ccg gcg gcc agc gcg tgt gct	52
Met Ala Pro Ala Ala Ser Ala Cys Ala	
1 5	
ggg gcg cct ggc tcc cac ccg gcc acc acg atc ttc gtg tgt ctt ttt	100
Gly Ala Pro Gly Ser His Pro Ala Thr Thr Ile Phe Val Cys Leu Phe	
10 15 20 25	
ctc atc att tac tgc cca gac cgt gcc agt gcc atc cag gtg acc gtg	148
Leu Ile Ile Tyr Cys Pro Asp Arg Ala Ser Ala Ile Gln Val Thr Val	
30 35 40	
cct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg aca cta cac	196
Pro Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu His	
45 50 55	
tgc acc tac cag atg agc aat acc ctc aca gcc cct atc gtg atc tgg	244
Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Ala Pro Ile Val Ile Trp	
60 65 70	
aag tat aag tcg ttc tgt cgg gac cgt gtt gcc gac gcc ttc tcc cct	292
Lys Tyr Lys Ser Phe Cys Arg Asp Arg Val Ala Asp Ala Phe Ser Pro	
75 80 85	
gcc agc gtg gac aac cag ctc aac gcc cag ctg gcg gct ggc aac ccc	340
Ala Ser Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro	
90 95 100 105	
ggc tac aac ccc tat gtg gag tgc cag gac agc gta cgc act gtc agg	388
Gly Tyr Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg	
110 115 120	
gtg gtg gcc acc aaa cag ggc aat gct gtg acc ctg gga gac tac tac	436
Val Val Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr	
125 130 135	
cag ggc agg aga atc acc atc aca gga aat gct ggc ctg acc ttc gag	484
Gln Gly Arg Arg Ile Thr Ile Thr Gly Asn Ala Gly Leu Thr Phe Glu	
140 145 150	
cag acg gcc tgg gga gac agt gga gtg tat tac tgc tcc gtg gtc tca	532
Gln Thr Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser	
155 160 165	
gcc caa gat ctg gat ggg aac aac gag gcg tac gca gag ctc att gtc	580
Ala Gln Asp Leu Asp Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val	
170 175 180 185	
ctt gtt tat gct gct ggc aaa gca gcc acc tca ggt gtg cca agc atc	628
Leu Val Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile	
190 195 200	

tat gcc ccc agc atc tat acc cac ctc tct cct gcc aag act ccg cca Tyr Ala Pro Ser Ile Tyr Thr His Leu Ser Pro Ala Lys Thr Pro Pro	676
205 210 215	
cct ccg cct gcc atg att ccc atg cgt cct ccc tat ggg tac cct gga Pro Pro Pro Ala Met Ile Pro Met Arg Pro Pro Tyr Gly Tyr Pro Gly	724
220 225 230	
gac ttt gac agg acc agc tca gtt ggt ggc cac agc tcc cag gtg ccc Asp Phe Asp Arg Thr Ser Ser Val Gly Gly His Ser Ser Gln Val Pro	772
235 240 245	
ctg ctg cgt gaa gtg gat ggg agc gta tct tca gaa gta cga agt ggc Leu Leu Arg Glu Val Asp Gly Ser Val Ser Ser Glu Val Arg Ser Gly	820
250 255 260 265	
tac agg atc cag gct aac cag caa gat gac tcc atg agg gtc cta tac Tyr Arg Ile Gln Ala Asn Gln Gln Asp Asp Ser Met Arg Val Leu Tyr	868
270 275 280	
tat atg gag aag gag cta gcc aac ttc gat cct tcc cgg cct ggc cct Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro	916
285 290 295	
ccc aat ggc cga gtg gaa cgg gcc atg agt gaa gta acc tcc ctc cat Pro Asn Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser Leu His	964
300 305 310	
gaa gat gac tgg cga tct cgg cct tcc agg gct cct gcc ctc aca ccc Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala Leu Thr Pro	1012
315 320 325	
atc agg gat gag gag tgg aat cgc cac tcc cct cgg agt ccc aga aca Ile Arg Asp Glu Glu Trp Asn Arg His Ser Pro Arg Ser Pro Arg Thr	1060
330 335 340 345	
tgg gag cag gaa ccc ctt caa gaa cag cca agg ggt ggt tgg ggg tct Trp Glu Gln Glu Pro Leu Gln Glu Gln Pro Arg Gly Gly Trp Gly Ser	1108
350 355 360	
ggg cgg cct cgg gcc cgc tct gtg gat gct cta gat gac atc aac cgg Gly Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Ile Asn Arg	1156
365 370 375	
cct ggc tcc act gaa tca gga agg tct tct ccc cca agt agt gga cgg Pro Gly Ser Thr Glu Ser Gly Arg Ser Ser Pro Pro Ser Ser Gly Arg	1204
380 385 390	
aga ggg cgg gcc tat gca cct ccg aga agt cgc agc cgg gat gac ctc Arg Gly Arg Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu	1252
395 400 405	
tat gac ccc gac gat cct aga gac ttg cca cat tcc cga gat ccc cac Tyr Asp Pro Asp Asp Pro Arg Asp Leu Pro His Ser Arg Asp Pro His	1300
410 415 420 425	
tat tat gat gat ttg agg tct agg gat cca cgt gct gac ccc aga tcc	1348

Tyr Tyr Asp Asp Leu Arg Ser Arg Asp Pro Arg Ala Asp Pro Arg Ser	
430 435 440	
cgt cag cga tcc cac gat cct cgg gat gct ggc ttc agg tca cgg gac	1396
Arg Gln Arg Ser His Asp Pro Arg Asp Ala Gly Phe Arg Ser Arg Asp	
445 450 455	
cct cag tat gat ggg cga ctc tta gaa gag gct tta aag aaa aaa ggg	1444
Pro Gln Tyr Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys Lys Lys Gly	
460 465 470	
gct ggg gag aga aga cgc gtt tac agg gag gaa gaa gaa gaa gag	1492
Ala Gly Glu Arg Arg Arg Val Tyr Arg Glu Glu Glu Glu Glu Glu	
475 480 485	
gag ggc cac tat ccc cca gca cct ccg cct tac tct gag act gac tcg	1540
Glu Gly His Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser	
490 495 500 505	
cag gcc tcg agg gag cgg agg atg aaa aag aat ttg gcc ctg agt cgg	1588
Gln Ala Ser Arg Glu Arg Arg Met Lys Lys Asn Leu Ala Leu Ser Arg	
510 515 520	
gaa agt tta gtc gtc tga tcccacgttt tgttatgtag cttttatact	1636
Glu Ser Leu Val Val *	
525	
tttttaattg gaatattgat gaaactcttc accaagccta ataaaa	1682

<210> 16
 <211> 594
 <212> PRT
 <213> Mus musculus

<400> 16	
Met Ala Pro Ala Ala Ser Ala Cys Ala Gly Ala Pro Gly Ser His Pro	
1 5 10 15	
Ala Thr Thr Ile Phe Val Cys Leu Phe Leu Ile Ile Tyr Cys Pro Asp	
20 25 30	
Arg Ala Ser Ala Ile Gln Val Thr Val Pro Asp Pro Tyr His Val Val	
35 40 45	
Ile Leu Phe Gln Pro Val Thr Leu His Cys Thr Tyr Gln Met Ser Asn	
50 55 60	
Thr Leu Thr Ala Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg	
65 70 75 80	
Asp Arg Val Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu	
85 90 95	
Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu	

100					105					110					
Cys	Gln	Asp	Ser	Val	Arg	Thr	Val	Arg	Val	Val	Ala	Thr	Lys	Gln	Gly
		115					120					125			
Asn	Ala	Val	Thr	Leu	Gly	Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	Ile
		130				135					140				
Thr	Gly	Asn	Ala	Gly	Leu	Thr	Phe	Glu	Gln	Thr	Ala	Trp	Gly	Asp	Ser
					150					155					160
Gly	Val	Tyr	Tyr	Cys	Ser	Val	Val	Ser	Ala	Gln	Asp	Leu	Asp	Gly	Asn
				165					170					175	
Asn	Glu	Ala	Tyr	Ala	Glu	Leu	Ile	Val	Leu	Gly	Arg	Thr	Ser	Glu	Ala
				180				185					190		
Pro	Glu	Leu	Leu	Pro	Gly	Phe	Arg	Ala	Gly	Pro	Leu	Glu	Asp	Trp	Leu
				195			200					205			
Phe	Val	Val	Val	Val	Cys	Leu	Ala	Ser	Leu	Leu	Phe	Phe	Leu	Leu	Leu
				210		215				220					
Gly	Ile	Cys	Trp	Cys	Gln	Cys	Cys	Pro	His	Thr	Cys	Cys	Cys	Tyr	Val
				225		230				235					240
Arg	Cys	Pro	Cys	Cys	Pro	Asp	Lys	Cys	Cys	Cys	Pro	Glu	Ala	Leu	Tyr
				245				250						255	
Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	Pro
				260				265					270		
Ser	Ile	Tyr	Thr	His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro	Pro	Pro
				275			280				285				
Ala	Met	Ile	Pro	Met	Arg	Pro	Pro	Tyr	Gly	Tyr	Pro	Gly	Asp	Phe	Asp
				290		295				300					
Arg	Thr	Ser	Ser	Val	Gly	Gly	His	Ser	Ser	Gln	Val	Pro	Leu	Leu	Arg
				305		310				315					320
Glu	Val	Asp	Gly	Ser	Val	Ser	Ser	Glu	Val	Arg	Ser	Gly	Tyr	Arg	Ile
				325				330						335	
Gln	Ala	Asn	Gln	Gln	Asp	Asp	Ser	Met	Arg	Val	Leu	Tyr	Tyr	Met	Glu
				340				345					350		
Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser	Arg	Pro	Gly	Pro	Pro	Asn	Gly
				355			360					365			
Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val	Thr	Ser	Leu	His	Glu	Asp	Asp
				370		375				380					
Trp	Arg	Ser	Arg	Pro	Ser	Arg	Ala	Pro	Ala	Leu	Thr	Pro	Ile	Arg	Asp
				385		390				395					400
Glu	Glu	Trp	Asn	Arg	His	Ser	Pro	Arg	Ser	Pro	Arg	Thr	Trp	Glu	Gln

405					410					415					
Glu	Pro	Leu	Gln	Glu	Gln	Pro	Arg	Gly	Gly	Trp	Gly	Ser	Gly	Arg	Pro
			420					425					430		
Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp	Asp	Ile	Asn	Arg	Pro	Gly	Ser
			435				440					445			
Thr	Glu	Ser	Gly	Arg	Ser	Ser	Pro	Pro	Ser	Ser	Gly	Arg	Arg	Gly	Arg
			450				455					460			
Ala	Tyr	Ala	Pro	Pro	Arg	Ser	Arg	Ser	Arg	Asp	Asp	Leu	Tyr	Asp	Pro
465					470					475					480
Asp	Asp	Pro	Arg	Asp	Leu	Pro	His	Ser	Arg	Asp	Pro	His	Tyr	Tyr	Asp
				485					490						495
Asp	Leu	Arg	Ser	Arg	Asp	Pro	Arg	Ala	Asp	Pro	Arg	Ser	Arg	Gln	Arg
			500					505						510	
Ser	His	Asp	Pro	Arg	Asp	Ala	Gly	Phe	Arg	Ser	Arg	Asp	Pro	Gln	Tyr
		515					520					525			
Asp	Gly	Arg	Leu	Leu	Glu	Glu	Ala	Leu	Lys	Lys	Lys	Gly	Ala	Gly	Glu
	530					535						540			
Arg	Arg	Arg	Val	Tyr	Arg	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	His
545					550					555					560
Tyr	Pro	Pro	Ala	Pro	Pro	Pro	Tyr	Ser	Glu	Thr	Asp	Ser	Gln	Ala	Ser
				565					570					575	
Arg	Glu	Arg	Arg	Met	Lys	Lys	Asn	Leu	Ala	Leu	Ser	Arg	Glu	Ser	Leu
			580					585					590		
Val	Val														

<210> 17
 <211> 575
 <212> PRT
 <213> Mus musculus

<400> 17
 Met Ala Pro Ala Ala Ser Ala Cys Ala Gly Ala Pro Gly Ser His Pro
 1 5 10 15
 Ala Thr Thr Ile Phe Val Cys Leu Phe Leu Ile Ile Tyr Cys Pro Asp
 20 25 30
 Arg Ala Ser Ala Ile Gln Val Thr Val Pro Asp Pro Tyr His Val Val
 35 40 45
 Ile Leu Phe Gln Pro Val Thr Leu His Cys Thr Tyr Gln Met Ser Asn
 50 55 60

Thr	Leu	Thr	Ala	Pro	Ile	Val	Ile	Trp	Lys	Tyr	Lys	Ser	Phe	Cys	Arg	65	70	75	80
Asp	Arg	Val	Ala	Asp	Ala	Phe	Ser	Pro	Ala	Ser	Val	Asp	Asn	Gln	Leu	85	90	95	
Asn	Ala	Gln	Leu	Ala	Ala	Gly	Asn	Pro	Gly	Tyr	Asn	Pro	Tyr	Val	Glu	100	105	110	
Cys	Gln	Asp	Ser	Val	Arg	Thr	Val	Arg	Val	Val	Ala	Thr	Lys	Gln	Gly	115	120	125	
Asn	Ala	Val	Thr	Leu	Gly	Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	Ile	130	135	140	
Thr	Gly	Asn	Ala	Gly	Leu	Thr	Phe	Glu	Gln	Thr	Ala	Trp	Gly	Asp	Ser	145	150	155	160
Gly	Val	Tyr	Tyr	Cys	Ser	Val	Val	Ser	Ala	Gln	Asp	Leu	Asp	Gly	Asn	165	170	175	
Asn	Glu	Ala	Tyr	Ala	Glu	Leu	Ile	Val	Leu	Asp	Trp	Leu	Phe	Val	Val	180	185	190	
Val	Val	Cys	Leu	Ala	Ser	Leu	Leu	Phe	Phe	Leu	Leu	Leu	Gly	Ile	Cys	195	200	205	
Trp	Cys	Gln	Cys	Cys	Pro	His	Thr	Cys	Cys	Cys	Tyr	Val	Arg	Cys	Pro	210	215	220	
Cys	Cys	Pro	Asp	Lys	Cys	Cys	Cys	Pro	Glu	Ala	Leu	Tyr	Ala	Ala	Gly	225	230	235	240
Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Ile	Tyr	245	250	255	
Thr	His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro	Pro	Pro	Ala	Met	Ile	260	265	270	
Pro	Met	Arg	Pro	Pro	Tyr	Gly	Tyr	Pro	Gly	Asp	Phe	Asp	Arg	Thr	Ser	275	280	285	
Ser	Val	Gly	Gly	His	Ser	Ser	Gln	Val	Pro	Leu	Leu	Arg	Glu	Val	Asp	290	295	300	
Gly	Ser	Val	Ser	Ser	Glu	Val	Arg	Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Asn	305	310	315	320
Gln	Gln	Asp	Asp	Ser	Met	Arg	Val	Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	325	330	335	
Ala	Asn	Phe	Asp	Pro	Ser	Arg	Pro	Gly	Pro	Pro	Asn	Gly	Arg	Val	Glu	340	345	350	
Arg	Ala	Met	Ser	Glu	Val	Thr	Ser	Leu	His	Glu	Asp	Asp	Trp	Arg	Ser	355	360	365	

Arg Pro Ser Arg Ala Pro Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp
 370 375 380
 Asn Arg His Ser Pro Arg Ser Pro Arg Thr Trp Glu Gln Glu Pro Leu
 385 390 395 400
 Gln Glu Gln Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro Arg Ala Arg
 405 410 415
 Ser Val Asp Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser Thr Glu Ser
 420 425 430
 Gly Arg Ser Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg Ala Tyr Ala
 435 440 445
 Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro Asp Asp Pro
 450 455 460
 Arg Asp Leu Pro His Ser Arg Asp Pro His Tyr Tyr Asp Asp Leu Arg
 465 470 475 480
 Ser Arg Asp Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg Ser His Asp
 485 490 495
 Pro Arg Asp Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr Asp Gly Arg
 500 505 510
 Leu Leu Glu Glu Ala Leu Lys Lys Lys Gly Ala Gly Glu Arg Arg Arg
 515 520 525
 Val Tyr Arg Glu Glu Glu Glu Glu Glu Glu Glu Gly His Tyr Pro Pro
 530 535 540
 Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg
 545 550 555 560
 Arg Met Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val Val
 565 570 575

<210> 18
 <211> 526
 <212> PRT
 <213> Mus musculus

<400> 18
 Met Ala Pro Ala Ala Ser Ala Cys Ala Gly Ala Pro Gly Ser His Pro
 1 5 10 15
 Ala Thr Thr Ile Phe Val Cys Leu Phe Leu Ile Ile Tyr Cys Pro Asp
 20 25 30
 Arg Ala Ser Ala Ile Gln Val Thr Val Pro Asp Pro Tyr His Val Val
 35 40 45

Ile	Leu	Phe	Gln	Pro	Val	Thr	Leu	His	Cys	Thr	Tyr	Gln	Met	Ser	Asn	
50						55					60					
Thr	Leu	Thr	Ala	Pro	Ile	Val	Ile	Trp	Lys	Tyr	Lys	Ser	Phe	Cys	Arg	
65					70					75					80	
Asp	Arg	Val	Ala	Asp	Ala	Phe	Ser	Pro	Ala	Ser	Val	Asp	Asn	Gln	Leu	
				85					90					95		
Asn	Ala	Gln	Leu	Ala	Ala	Gly	Asn	Pro	Gly	Tyr	Asn	Pro	Tyr	Val	Glu	
		100						105					110			
Cys	Gln	Asp	Ser	Val	Arg	Thr	Val	Arg	Val	Val	Ala	Thr	Lys	Gln	Gly	
		115					120					125				
Asn	Ala	Val	Thr	Leu	Gly	Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	Ile	
	130					135					140					
Thr	Gly	Asn	Ala	Gly	Leu	Thr	Phe	Glu	Gln	Thr	Ala	Trp	Gly	Asp	Ser	
145					150					155					160	
Gly	Val	Tyr	Tyr	Cys	Ser	Val	Val	Ser	Ala	Gln	Asp	Leu	Asp	Gly	Asn	
				165					170					175		
Asn	Glu	Ala	Tyr	Ala	Glu	Leu	Ile	Val	Leu	Val	Tyr	Ala	Ala	Gly	Lys	
		180						185					190			
Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Ile	Tyr	Thr	
		195					200					205				
His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro	Pro	Pro	Ala	Met	Ile	Pro	
	210					215					220					
Met	Arg	Pro	Pro	Tyr	Gly	Tyr	Pro	Gly	Asp	Phe	Asp	Arg	Thr	Ser	Ser	
225					230					235					240	
Val	Gly	Gly	His	Ser	Ser	Gln	Val	Pro	Leu	Leu	Arg	Glu	Val	Asp	Gly	
				245					250					255		
Ser	Val	Ser	Ser	Glu	Val	Arg	Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Asn	Gln	
			260					265					270			
Gln	Asp	Asp	Ser	Met	Arg	Val	Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	Ala	
	275						280					285				
Asn	Phe	Asp	Pro	Ser	Arg	Pro	Gly	Pro	Pro	Asn	Gly	Arg	Val	Glu	Arg	
	290					295					300					
Ala	Met	Ser	Glu	Val	Thr	Ser	Leu	His	Glu	Asp	Asp	Trp	Arg	Ser	Arg	
305					310					315					320	
Pro	Ser	Arg	Ala	Pro	Ala	Leu	Thr	Pro	Ile	Arg	Asp	Glu	Glu	Trp	Asn	
				325					330					335		
Arg	His	Ser	Pro	Arg	Ser	Pro	Arg	Thr	Trp	Glu	Gln	Glu	Pro	Leu	Gln	
			340					345					350			

Glu Gln Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro Arg Ala Arg Ser
 355 360 365
 Val Asp Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser Thr Glu Ser Gly
 370 375 380
 Arg Ser Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg Ala Tyr Ala Pro
 385 390 395 400
 Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro Asp Asp Pro Arg
 405 410 415
 Asp Leu Pro His Ser Arg Asp Pro His Tyr Tyr Asp Asp Leu Arg Ser
 420 425 430
 Arg Asp Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg Ser His Asp Pro
 435 440 445
 Arg Asp Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr Asp Gly Arg Leu
 450 455 460
 Leu Glu Glu Ala Leu Lys Lys Lys Gly Ala Gly Glu Arg Arg Arg Val
 465 470 475 480
 Tyr Arg Glu Glu Glu Glu Glu Glu Glu Gly His Tyr Pro Pro Ala
 485 490 495
 Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg
 500 505 510
 Met Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val Val
 515 520 525

<210> 19
 <211> 22976
 <212> DNA
 <213> Homo sapiens

<220>

<221> exon
 <222> 1898..2253

<221> exon
 <222> 3437..3781

<221> exon
 <222> 12065..12184

<221> exon
 <222> 15045..15101

<221> exon
 <222> 15666..15812

<221> exon
 <222> 19479..19652

 <221> exon
 <222> 19799..19858

 <221> exon
 <222> 19956..20087

 <221> exon
 <222> 20229..20854

 <221> exon
 <222> 20944..21094

 <221> Misc_Feature
 <222> 19956..19958
 <223> Potential variant splicing site AAG

<400> 19
 aacagtttgg cagttcctca aaaggttaaa aatagaacta ccaagtcacc cagcaattcc 60
 attcttaggc atatattcaa aagaaatgaa agcagatatt tgtacaccag tgttcacagc 120
 tgcactattht acaatagtca aaaggtagaa acaacctagg tccatccaca aatgaatgga 180
 taaataaaaac gtagcatata catacaatgg tacactagtc cgctgtaaaa agaaatthtg 240
 atcttactgc atgctacatg gcttcgacat actacaacat ggatggacct tgaaaacatt 300
 attctthtggtg aaataaaacta gacacaggac aaatgttaga cgattccact tatatgaggc 360
 acctagaatg ggcaatthtg taagcaaagt agaatagaaa ttactagggg cacaggtagc 420
 agggaatggg gagttactgt ttaatgggtca cagagthtat gttggggatg atgaaacagt 480
 ttcggggata aagagtgggtg attggtacac gacattgtga atatacttaa tgccactgaa 540
 thttacactt gaagtgggtta aagcgataaa tattatagtt tgcatathtt atcataaaaa 600
 taththththta aacgatgaag ggacgtgaac gggthtgaaat thtataaaaa gtggccaggg 660
 aaggtgtcac tgcaatgggtg tcctacagga ggaggaagat catgtggaca tctgcgggaa 720
 ggggtgttctg gcagagggag tagcacgggc gatggctctg aggactgtga gaagtatagt 780
 tggaacacagc gaggaggcca ggggtgtccga agctgagtaa gccagagaga gtgggaggag 840
 gtgagataag agggggaagg tcagthtctg ctgagagtga ggaggagcca caggagggt 900
 gtgagcaggt ggacgtgatc tggcttgagt thtaacaggg ccagtagaac aaagcacgcc 960
 tgggtaccga aaccagccac tggccagttg gcaacctggg ggagtctaac gcgaggaagc 1020
 gcccagggtt cccccaggat gcgctthccc tcgccgccac ctggagacag cagagtcacg 1080

cccagcgctg cgcaggctga tcgccgcgcc gcgccccgc cctcggtcgc aggtggctcg	1140
ttccgggaat tcctaagcgg aaaccgggtcc caagccccgc gccttcgctc ggccccctta	1200
agagccagaa tttccggagg gctgacccgg gggctagggg tgcccagggg ccgaaccaca	1260
agttgggaac ggggtggggg ggtggcgaaa acttccgaag tggaattcca acttttcctg	1320
gccctgattc cccttgggca tccctgaggg ggcagagctt cccttcgggg gacttttagag	1380
ggttcctcag gtcattctaac tgggagacac aggaggcccc aagcgcccc cctccacccg	1440
gtccggagga accccagtgg aagtggagaa gtcaggcgcc accaacaagc ctctcccagc	1500
caggactttg cttagactcg ctccctcccg cagggcgcac ctaggcgggt ccatcgccag	1560
ccggggagag gggtttgggc agggagggaa caggtgcgcg gcgggacccg ccctatctca	1620
acaggtgaat cgctccaagt gggctctcgg tgcattggatc tcgggtgcgt tggtttggcc	1680
ggagcagatg ggggccggaa gggacctgtg gtccgcaggc gccctcccag cgggccagtc	1740
acttggttcg ggccctgggg gacggagcgc acctgggtca gccacttcc ggggagggag	1800
gcagaggaac ccctccccgc cgctcacccc taagcccagc cctcggctcc cacccttgtg	1860
tacctgggcc gaaccattca ccggagcgcg cagcgggtgg agtgtggctc ggaggaccgc	1920
ggcgggtcaa gcacctttct ccccatatc tgaaagcatg ccctttgtcc acgtcgttta	1980
cgctcattaa aacttccaga atgcaacagg acggacttgg agtagggaca aggaacggaa	2040
gtgggaaggg gaggagcgtg caccctcctt ggccttgggt cgcgccgcgc ccctaaggt	2100
actttggaag ggacgcgcgg gccagacgcg cccagacggc cgcgatggcg ctggtggccg	2160
gcgggctctc cagagggctg ggctcccacc cggccgcgc aggccgggac gcggtcgtct	2220
tcgtgtggct tctgcttagc acctgggtgca caggtacggg gcacggggcc tctgacgctg	2280
cggaaacgcc gagggaactg tagaggggga tggatggagt tggaggcggc gggaaagcggg	2340
aagcgggggt ctcagaggct gggaccttcc gatccccctg gtcttgggcg atctgttgcg	2400
cgcgggagtg agaggaattc cccatttgtg ccggggagcg ctccccgcgc ccttatctgg	2460
aagatagcag gaagtgaaac tccctggacg gtgagacccg gagcggcagg gagaatggaa	2520
ctctttgtgg ggaggagtg gaagaccgcc cgatctctgg gaaaagaaaa gccgggatgg	2580
gacttgggcg caccggggga tttctaagtt ttggagtaac ggggagaggg cacgggaggg	2640
ctggatcaga cgcttcctag agggacagag acgaaggaac aatgcctagg cctcgggtgg	2700
gtgtgggact ggggactccc catccccgc accccacca cctccgcgg gctccggatt	2760
atacgtgcgt aagagtctgg tgggatggat ttacggactt gaaaccgact tctgctggca	2820

ggctttcacc	tggatgggat	atttgggtgg	tgatgaggtc	tttcccgaga	cacttttggt	2880
tcagtcattt	gaaatgactt	tagagtaggg	tgaggtggtg	ggaggctgat	ggagatattg	2940
tgggggcttt	agtccctcca	tggcaaagca	gttcaggcaa	acaactccat	ggttttccct	3000
ccaaattcaa	aaggccccgg	gtaacctgga	atccttcgta	gtcggttttg	aagtggggcc	3060
ttgggcgctg	ggggcatcaa	catggccatc	tgggcttgcc	tgcccaggcc	acacagaggc	3120
cccttgttgt	gggtgaatgg	caaaggggaag	aggggactgg	tgtggttcag	aggccacagg	3180
ctgggaagag	ggatggcggg	cgagtccaag	gaaactggcc	gtgtcaccgt	gcacctgcca	3240
cttcagcccc	acgggtctat	aaaatgggca	tgattatcgt	ggctacctca	ctggtcctgg	3300
caattaagga	acaatgtgtg	ccaggcactc	tgtaaaccac	atacttgcca	gtgtcaagct	3360
ggtgacaggt	ggcgttcctg	ttgaagcacc	tccctgagct	cacagcaacc	cttgctgtct	3420
ctcctcttgc	cctcagctcc	tgccagggcc	atccaggtga	ccgtgtccaa	cccctaccac	3480
gtggtgatcc	tcttccagcc	tgtgaccctg	ccctgtacct	accagatgac	ctcgaccccc	3540
acgcaaccca	tcgtcatctg	gaagtacaag	tctttctgcc	gggaccgcat	cgccgatgcc	3600
ttctccccgg	ccagcgtcga	caaccagctc	aatgcccagc	tggcagccgg	gaacccaggc	3660
tacaaccctt	acgttgagtg	ccaggacagc	gtgcgcaccg	tcagggtcgt	ggccaccaag	3720
cagggcaacg	ctgtgaccct	gggagattac	taccagggcc	ggaggattac	catcacccga	3780
agtatgttgg	gcagggcagg	gggatgaggc	tgggcttgcc	cgggtggtgg	gactggcgtc	3840
cttgtgcggg	acctggagtc	cccatctgaa	agctcttgag	tgccagtgtc	tgaaaggacc	3900
attgaaggga	gcaattcttt	tttttttttt	ttttgaagat	ggagtcttgc	tctggactcc	3960
aggctggagt	gcagtgggtg	gatctcagct	cactgcaacc	tccacctccc	aggttcaagc	4020
aattctcttg	cctcagcctc	ccgagtagct	gggactccag	gtgcgtgcca	ccacgcccag	4080
ttaatttttg	tatttttagt	agagatgggg	tttcaccatg	ttggccaggc	tggtctcaaa	4140
ctcctgacct	caaatgatct	gcccgccttg	gcctcgcaaa	gtgctgagag	acaccatacc	4200
cagcctaaag	ggagcgattc	tattctacta	ttcttccttc	tgctaatacct	tccattcttt	4260
aatttaataa	cgaagatttt	ttgagtacct	gtcatatacc	aggtgctggt	ctgggccctg	4320
ggaatacagc	tgtaacaaaa	atcatcaaac	cacttccttc	gtggagccca	cattgcagtg	4380
agagagacaa	acacgacaca	cactctcaag	tccttgaaga	taaagaaaac	tgggtaacgg	4440
agagaagagg	ccagggtttg	ttctataatc	attaataaca	cgagcagtaa	gaagtaaaat	4500

ttatctaagt	aacaacttat	aaaggggtcta	ctgtgtgcta	agctctcatc	caggttccca	4560
aggattaact	cagaccacac	agtaattgaa	tagattctat	cattgtcatc	ttacagaggc	4620
ccagagagag	aaagtgactt	gcctagtgtc	atagctggta	acggggctgg	gattctaact	4680
cagccacttt	gggtctagt	gccaagctcc	taatcccttt	gcttgccctag	ggtgggtccgc	4740
agaggactca	cagaggagat	ggcaggagt	aactgcaggg	gcaagagagc	ttaatggaga	4800
aagcctgtga	catgccagga	actgcacaca	tattctccca	ttgagtcctc	tcctctaccc	4860
tcctgacagc	tgaggcacag	agaggttacc	ttgttcaa	gggtgcatag	gaagtcaaag	4920
tctggagctg	gggtttgaac	ccaggcagcc	ctgagaacct	tgttcttttt	ttttgagacg	4980
gagtctcgct	ctgtcgccca	ggctggagt	cagtggcggg	atctcggctc	actgcaactc	5040
cgctccccgg	gttcacgcca	ttctcctgcc	tcagcctccc	aagtagctgg	gactacaggc	5100
gcccgcact	acgcccggct	aattttttgt	atttttagta	gagacgggg	ttcaccgttt	5160
tagccgggat	ggtctcgatc	tcctgacctc	gtgatccgcc	cgctcggcc	tcccaaagt	5220
ctgggattac	aggcgtgagc	caccgcgcc	ggccccctgt	tcttaactgt	aatgctgcct	5280
cctgatagga	tgtgcctgtt	gggactaagt	aaggggcagt	cattcattca	ttcatttggt	5340
atttatcaag	catcgactat	gtgtcgttgg	tgctggggat	agaggtgatt	gggatggctg	5400
aagtttctgt	cgtcaaggag	atgacattct	ggtggagtga	gactggcagt	aaataagcag	5460
ataaagaaag	agtatgagaa	tttcaaagtc	tgggcacgg	ggctcacgtc	tgtaatctca	5520
gcactttggg	aggccaagg	gggtggatca	cctgagggtca	ggagtccag	accagcctgg	5580
ccaacatgg	gaaaccccgt	ctctactaaa	aatacaaaga	ttagccaggc	atggtggcac	5640
atgcctgtaa	tcccagctac	tcaggaggct	gaggcatgag	aatcgcttga	accagggagg	5700
cagaggttgc	agtgagctga	gatcgcacca	ctgtactgca	gtctgggcga	cagagtgaga	5760
ctctgtctca	aaaaaaaaaa	aaaaaaaaaa	gactccgtca	aggtataaga	atgtcagaga	5820
gtactaagt	ttgcaaagaa	aataacacca	ggctgggtgc	attggctcat	gcctgtaa	5880
ttcagcactt	tgggaggcca	aggcaggagg	atcacttgag	cctaggagtt	tgagaccagc	5940
ctggacaaca	aatgagacc	ccatgtctac	aaaaatttta	aaaatttaaa	aattagctgg	6000
gcatgggtgg	atgtgcctgt	ggtccccgg	gctcaggagg	ctgagggtgg	aggattgctt	6060
gggcttgaga	ggtcaaggct	tcagtgagtc	atgatcgtgc	cactgcattc	cagcctgggt	6120
gacagagtga	gaccctgtct	tgaaatgaaa	agaaaatagg	ctgggcgcag	tggctcacac	6180
ctgtaatccc	agcactttgg	gaggccgagg	tgggtggatc	acctgaggtc	aggagatcga	6240

gaccagcctg gccaacatgg tgaaatccca tctctactaa aaatacaaaa tttagccggg	6300
cgtggtggtg ggcgcctgta atcccagcta ctcgggagggc tgaggcagga gaatcgcttg	6360
aacctgggag gcgaagggtt cggtgcgcca agattgcgcc actgcactct agcctgggaa	6420
acagtgagac tccgtcttaa aaaaaaaga aaaaagaaaa tagcactggg tgatgtgcta	6480
catggaatga cttgggctgt gaatatgatt tgaggagggc ctgggcctgg gccttacaga	6540
acctagaagg cagagaggaa ggggaggggc agggtgccag ggatgaaggc tcacgtacct	6600
catgtcttag tgtgtgttca ctgtcttaaa caagaattta aagttgggca tggggcagag	6660
cggggaaggg agcatccctt tgcagacccc aagaagccag gaactggagc acattctgct	6720
agaggatcga tgggaagcag ggttccaggg gctgagccta tgtcagtcct gtttcagagg	6780
aggcaccagg cttgcttgcc ctgaatttct gtgggcagct cagccatgag catcctactg	6840
ttattgaggt cacagggctg cttaggcccc ctctctctta acccagggat tgtgcctgcc	6900
tggaccaggc gtgactgcta agcttctgcc aggacaagcc aaatactgag ggtgcttcct	6960
ctgctggacg caaaagtcca ggatgacccc ccaggctctg tctcggggaa ggggccctgc	7020
atgctccagg ggcctcacag gcctgggtct ttcaaaccac cccacctgg gcctgtgttt	7080
gatcaaggcc ctgagtgtaa acatccattg tgtgtgtcct ttcaggaaat cccatagcca	7140
taggagcttc ctctgtttca gctttgagga tggggaaaag tggactcccc gtggtgttcc	7200
tagggtcacc cactgtgctg gggtttttct gttgttggtg ttttttttct gttgcccagg	7260
ctggagtgca gtggtgcaat ctcagctcac tgcaacctct gcctcgcaag ttcaagtgat	7320
tctccgcctc agcctcctga gtagctggga ttacaggtgc acaccaccac acctggctaa	7380
tttttgatc tttttggtag agatgggatt tcgccatgtt ggccaggctg gtctcaaact	7440
cctgacctca ggtgatctgc ctgccttggc ctcccaaagt tctgggatta cagatgtgag	7500
ccaccatgcc cggcctatcc tggtttcaaa agtgaaaata gtccctggata aggtagaagg	7560
ctgtccactc caggcatccc tccggtccgg tggctcattc cctgctttgt ccttccatgc	7620
tttgggtgat ggaccagcac ctggacagga ggcctgttc cacctcctcg ggctccttgg	7680
ggtccaagtg cccccacctc cagctgcact gcagcagaga gcccatggga cctctgaaat	7740
catgaaggtc acctttgcgg tgtataaaga aggaaccaga ggttggagat gtggaggagg	7800
cctggctgct gttcccactg gagacctggc atcttctccc cgacctaaaa caatgaaagc	7860
agtgtcagc ccggatgaga tcacggccag cccaagacca ggaacagggt acgccctgca	7920

ggaagaaggt	gtgcccagac	cttaggatgg	atcaaaagaa	gccggaaaac	tatatattttt	7980
gtgagttttg	aaaatgtcag	acaggtcaaa	caaaacacag	tgaggtccag	cctcggccta	8040
caagatgcca	gatttcaacc	cctggcctat	atgatctggt	tgccatggca	ggcggttcct	8100
gtccacctct	tttgtttata	gcagggacca	gctcttgagc	tccagtgttg	aagaggcacg	8160
gtcagggctc	gatctgaaga	cactgggtggc	tcatgcctgt	aatcccagca	cttcaggagg	8220
ccgaggcagg	aggattgctt	gaggacagga	gctgggagac	cagcctgggc	aacacagtga	8280
gacctcagaga	ctacaaaaaa	ataaatattag	cggggcatga	tggcacaccc	tgctactctg	8340
gagatgggaa	gattgcttga	gcctaggagt	tcgaagctgc	agtgacccat	gatcgcacca	8400
ctgcactcca	gcctggggcga	ccaagctagg	ccctctcaaa	aaagatacag	gtggaaaaat	8460
gatggacgaa	gagggcattg	tggcaaacct	ggggatttag	gagaacctag	tttggaattc	8520
tatgaggatt	caatgaaaga	atgtgtgtag	aggggcccag	cacatagtaa	gagctcaata	8580
aacggtgggg	gctaggggcg	gtggctcatg	cctgtaatcc	cagcactttg	ggaggctgag	8640
gcaggtggat	cacttgagcc	ctggagttca	agatcaacct	ggacaacaaa	gcaagatccc	8700
atctcaaaat	taaaaaacia	caccaacaac	aaaaaacacag	tggcttagat	gcctgatcat	8760
tagggtaagt	cgtgtcctca	accctttcac	atctgctctg	aaggtcacca	tatccggaag	8820
ccttccctgg	cctccttggt	taaaatggca	cagccccac	tccacgcctg	gcactctctg	8880
ctgtccctga	ttcgttttct	ccatacagct	tatctttgtc	tgatatgtga	catagttaac	8940
attttatatt	tgtctttctt	tcctagttag	aatctgaact	ctagaagggc	aagggaagg	9000
atttataact	caaaggttcc	gggcttaggc	ctcttttata	ttcttgattt	tgaggttaat	9060
taagagctca	ggcctagcga	ggtggctcat	gcctggaatc	ccagcacttt	gggaggccca	9120
ggcgggcaga	tcacttgagg	tcaggagttc	cagacctgcc	tggccaacac	agtgaaaaac	9180
ctgtctctac	taaaaataca	aaaattagcc	agttatgttg	gcaggcgcct	ataatcccag	9240
ctactcaaga	ggctgaggca	ggagaatcgc	ttgaaccacag	gaggcagagg	ctgcagtgag	9300
ccaagatcgt	gccactgcac	tccagcctgg	gcaacagagc	gagactccat	ctcaaaaaaa	9360
aaaaaaaaat	taagagctca	aagagtttgt	tttcataggc	agcagaatga	gaaaagttta	9420
caaaatagtt	taaatgacaa	taaagtcatt	atagattaac	ataaataaaa	taccttttat	9480
gaaaaaaata	atcattttct	gaaatcagac	aaaacattgt	gaatgagaag	gtggcatggc	9540
tttatatttt	tgcaagtctc	cgaagcctgg	ctggatagaa	gagcctggct	tctcagagct	9600
gcttcagtct	gttgtgatat	ctattgtatg	tcacgtagcc	tctggaaaac	tccacagtta	9660

gtattggttg	gaaaataact	ttgacctcag	gatctcctga	aaacgtcttg	gggaacccca	9720
gggtctagag	gctgcagttt	gagaactggt	gctgtggtat	cccaggtgtc	tcaaatactg	9780
cctagaacat	aggtggtact	cagtaattat	tgttgaagga	tgaatgaatg	aatgaatgaa	9840
tgaatgaatg	aaagaaagaa	agaaatgtgt	ctttgaatcc	agccatgtgc	ccagaatgat	9900
gagacagatg	acaaaagcta	agggacttta	gcatgaggag	aggggggttcg	tttcctttttt	9960
tttcctttttt	ttttgagatg	gagtctcact	ctactgccca	ggctagagtg	cagtgggtgca	10020
atctcagctc	actgcaatct	ctgcctcctg	agttcaagca	attctcctgc	ctcagcctcc	10080
agggtagctg	ggactacagg	tgcgtgccac	catgcctagc	taatttttta	catttttgggt	10140
agagatgggg	ttttaccatg	ttggccgggc	tggtctggaa	ctcctgacct	caagtgatcc	10200
acctgcctca	gcctcccaaa	gtgttaggat	tacaggtgtg	agccaccatg	tccggccaag	10260
aggggtgttca	tttctgctcc	ttgccaggta	ttgtgtcagg	cactggggac	ccagcagtgg	10320
ctgagacaga	cagggctctg	cctcacggag	cccacatttt	caccaggcaa	aggatgggtcg	10380
gcccctaagc	tgggagataa	gacttcagca	gttgggtggg	ggagccgtgg	gagaagccca	10440
gcccacaggg	ggacagtgca	aatctagaac	caaggcgatg	gcaggggtga	ggctggcacg	10500
gtagctagag	accacgtcgt	gccaagggcc	ttggggacca	tgggactatg	ggaccttagg	10560
gaaggcgtct	ggaatgctgt	agccagacac	tgttgcaagg	aggatttttc	tgtagacatg	10620
aggccttcct	tatgaagaaa	gcaagggttc	tttcattcct	gggggtgcca	ggtgctgtgg	10680
actgcagcac	gcgtgggttc	tgccgtcaca	gagctgtcat	gcaggagggc	agcgcgtcct	10740
tgggaagggtg	gcaggcaggt	caggctagga	ggaaagaggc	cgggaagctg	agggcatttc	10800
ctgcccgaga	tgcccaatgt	agcctacttc	tgtccccagt	ggcttaaggc	agagttgcct	10860
ggtaggtgcc	ctggtcccac	cctggtgaaa	ggctgaagggt	atttaattag	tgcctgagaa	10920
gcagagagga	aacaggatgt	gccaaaacac	tttgatggat	gtagagtta	acaggctcct	10980
tgcctgcagc	tgcttcagac	aagagcgtcc	ccaagccctg	ggcctgacct	ggaatgtggg	11040
gatggaaggg	gagggggagg	aaccaaggca	ctgggagggt	aagtctctct	ctcccacata	11100
gacacacca	ctccttatgg	gtgcctgggc	atctcctgggt	acctagaatc	tggcctgttt	11160
atctccacac	ccatccctgg	ggtctacact	aggccctgtg	ggtggcagtt	cacatcaggg	11220
gagttctgac	tttggctctg	agaggtgggt	cagagatggc	tgtaagttga	gaagcacaga	11280
ctgctgggtg	tggtgggttca	cgctgtaat	cccagcactt	tgggaggctg	aggtgggggt	11340

ggatcacctg aggtctggag ttcaaaacca acttgggtcaa catggcgaaa ctccatctct 11400
 actaaaaatg caaaaattag ccaggtgtgg tggcaggtgc ctataatccc agctacatgg 11460
 gaggctgagg caggagaatt gcttgaatct gggaggcgaa gattgtagtg agccgagatt 11520
 agttcgcacc attgcatgcc agcctgggca acaagagtga aactccgatt caaacaaaaa 11580
 aaaaaaaaaag ctgggcatgg tggagtgcct gtagtcctaa ctactcaggt gggaggattg 11640
 cttgagtcca ggaggttgaa gttgcagtgg gctataatta caccactgca ctccagccag 11700
 ggccacagag tgagaccctg tctctaaaga aagaaaaaaa aaaacaacct caggctccga 11760
 gggcaccatt actgctctat actgaagagc tgtgcagctt ttccagaccc gaaatgtcat 11820
 ccacaaaaca gaagtgataa tggtcctgcc tcacagactt cttgcagtag tccaggtggt 11880
 tagaacgggg tgtaaaaggc cgtgtgccct tggtaggaat ctttgcatat gcatttgatc 11940
 atctgcagcc tgcccagccc actgcttgcc ccctcctggg tgtgctggga aggggtcttt 12000
 ggccctccag gggtaggtg ccccagcctc caaggtgccc tcacgccttt tcatcccagc 12060
 tcagatgctg acctgacctt tgaccagacg gcgtgggggg acagtgggtg gtattactgc 12120
 tccgtgggtc cagcccagga cctccagggg aacaatgagg cctacgcaga gctcatcgtc 12180
 cttggtgagt gggcctggga agggggaggc atggcccttc cttttgtccg cttctgttct 12240
 gtctgccctc ccctgtgtcc gccctctgcc ctccagctta ccctctgggc tctgtcgctt 12300
 gctctgctct ccccaggct ctgccagtca cttaggctcc cctgtgccct gcaccccagg 12360
 cagggaccac tggcccacag tgcctccaat caccgaagcc aaactaagag aagagtggag 12420
 acaattggag actctgcctt ttcaaagtct catttttaaa aaaaatccag acttggggtc 12480
 cgggtgcggt agttcatgcc tgtaatccca gcactttggg aggccgaggc gggtaggatca 12540
 cttgaggcca ggagttcgag actagcctgg ccaacgtggc aaaatcccgt ctctataaaa 12600
 aatataaaaag ccaggcgtgg tgggtgcacat gcctgtaatc ccagttactc agaaggctga 12660
 ggcatgagga ttgcttgaac ctgggaggca gaggatgcag taagccaaga tcaagccact 12720
 gcactccagc ctgggcgaca gagtgagact ctgtccaaaa aaaaaaaaaa tccagacgtg 12780
 gtcagagtcc atgggcagtg aatgaggaca gttgatgggt tgcaaaatcg acccacctct 12840
 tgctacatcc ccaaggcctc atctcaccgg agtccctcgc caaagcacag cggttttgcc 12900
 gtgtgccctg ctgggatggc gctgcatggc acacacactg tgtaagtttg agtgcagctg 12960
 aaacgaagcc gattccagac acccaggggc agggcggggt gtccgtgtgg ctgggaggcc 13020
 tccttgtgtt agggggatgt tgccatcggc caggtgccct gctgtaagcc aacacatgga 13080

gtcttgtatg	acatgtgctc	tgcattgagt	atgccgctgg	gctgtacact	gccatcttca	13140
catgtgtgaa	tgagcacgtg	actggggggg	acttgggctg	caagacagag	ttcatgtgtg	13200
ggggatggaa	cacgtgcacc	agtgacccag	gaacctctgc	ctgttcttcg	gtaaaatgca	13260
ccatttgcac	cagcagttcc	caaaattagt	ctccaggtct	atttacactc	taaaacatta	13320
tcgaggggtc	ccaagagctt	ttgtttgttt	ctgtggggtt	tatgtctatc	tggttgctta	13380
catattagga	attaaaatgg	ggagattttc	cttttttttt	tttttttttg	agatggagtc	13440
tcgttctgtc	gcccaggctg	gagtgcagtg	gctcgatctc	ggctcactgc	aagcttcacc	13500
tcctgggttc	acgccattct	cctgcctcag	cctcccaggt	agctgggact	acaggcaccc	13560
gccaccacac	ccggctaatt	ttttttgtat	tttttagtag	gactggggtt	caccatgtta	13620
gccaggatgg	tctcgatctc	ctgacctcgt	gatccacca	cctgggcctc	ccaaagtgct	13680
gggattacag	gcatgagcca	ctgcccggcc	ttaaaatggg	gagatttttc	aagcccaaga	13740
tacacaagga	agactgggca	acatggcaag	accctgactc	tacaaaaaat	tttaaaatta	13800
accaggcatg	gtggcatgca	cctgtgagcc	cagcttcttg	ggaggctgag	gcaggagtat	13860
cgcttgcacc	caggaggtca	aggctgcagt	gagccgtgac	tatgctactg	cactctagca	13920
tgagtgcag	agaccctggc	tcaagaaaca	caaacacaca	cacacacaca	cacacgcata	13980
tagtccatta	ggcatcaggg	cgatgatggc	atcagggagc	ctgggaaact	ctactggaca	14040
ttcatgggag	aacaagtga	aaaggcaa	aacatcttag	tggtattcta	aaatttcttc	14100
ttttggcctt	gtggacagga	ccacgctttg	agagctgtga	ctgacatgcc	tctgtcctgt	14160
tgcgagggcc	tatagtgcca	agtgcatgag	ctctggggag	ggcttcgtgg	gtgcagagct	14220
gggcctgtgg	aggccctca	gacacaacac	tggtggggct	cagagctcca	ggggcactcg	14280
agggaagaca	agaaccggct	ctgagatgcg	tgaatgtgac	agtgcatgag	tagagatgga	14340
gaccttgtgg	gtcccagaac	caggactgca	tatgactttc	atatgtgggt	atttttgcct	14400
tcatgggtcc	cttctgtttt	taaaaaaaa	gtgtgattat	gttgtcaca	agagtttatt	14460
cctgtatatt	gtgttaattt	gtgttcagat	ttgtaaagta	aaattaaacc	atttcagcca	14520
ggtgtggtga	cacatgcctg	tagccctagc	tacttacc	agaggctgag	gtgggaggat	14580
cgcttgagcc	cacgaggttg	aagctgcagt	gagccatgat	cacaccctg	cactccagac	14640
tgggagacag	agctgagatc	ctatttcgtg	ggccctaggt	ccctgtgcct	gctggaacag	14700
gacatcccta	tcaccgtggg	tggagccctt	tgggggtgcta	agacctatga	atgagggaaa	14760

cttagggtgc	ccaagctgag	gtagagccct	cagaaccccc	tgggatttgt	attggagccc	14820
tcgtggcata	acacaggtgg	attatgcaat	gggagtttct	tacctataag	cacccacatg	14880
tgggcgggtg	gagggtagga	gccatgcact	agggcttcag	ccccagccc	cttcccgcct	14940
cagggcacac	cttgcacttg	gccagcctgg	agctgggcct	tcgggggtgg	cacagcctgg	15000
gctggctctg	gccagcataa	tctgtttctc	ttttgtccct	ccagggagga	cctcaggggt	15060
ggctgagctc	ttacctgggt	ttcaggcggg	gcccataгаа	ggtacggggg	gtggatcctg	15120
agttgggcct	ctcgggagct	cccatacatc	acctactgct	tctgactcta	gttagtatcc	15180
ccttccccac	taaaccctgc	tactgtgga	cccctcacta	acctggcctg	actgtggctc	15240
tgaggcatct	agtggctctg	cgctgggcct	aggctaggct	gggctgagga	gagcctgggg	15300
tgcaggccag	ggctctgtga	ctggcacctg	cggtgctctt	gagggtgtgg	cgtctgggca	15360
gctggctctc	tctttggctc	gggggctgca	gtctgtctcc	ctctgtgcag	gctgcctcgt	15420
tttctgcctt	gtgttttttg	cacctggggg	agggccgtaa	ctggggaatg	gccgggatgg	15480
tagaatgggg	agtgtgctgt	gccagcctc	tggcacaaaa	aatccagcca	gggctgcagg	15540
ttccttggtg	agctttgcaa	atcgtccccg	acctcagtgc	tggtcccgca	ccatgtaccc	15600
ctgctgtgcc	gtagccctg	ttccctccca	ggcctccggg	ctcagggcct	gttgtctttc	15660
tgcagactgg	ctcttcgtgg	ttgtggatat	cctggctgcc	ttcctcatct	tcctcctcct	15720
gggcatctgc	tggtgccagt	gctgcccgca	cacttgctgc	tgctacgtca	ggtgcccctg	15780
ctgcccagac	aagtgtgct	gccccgaggc	ccgtaagtgt	cccgtcatg	gccaccctgg	15840
tttgggcaac	atcctgcata	caagggaagg	aggtggccat	ccacctgccc	ccaggacagt	15900
ggcgttggtc	tggaggggtg	gaatttagcc	agtggggaga	aagtaggctg	aggagggctc	15960
gctgtttaga	ttgtcgttta	cttcctccaa	cttttagttt	atttttattt	atgttgttct	16020
tttcttttgt	aagtataatc	catacacatg	gtaaaaatgt	ccaacagtac	aagatactag	16080
tcacatggaa	gtaaagccct	ctaaaaaac	caaatcttgg	ctaggcgcag	tgattacgcc	16140
tgtaatccca	gcactttggg	aggccaagac	gagtggatca	cttgagggtca	ggagttccag	16200
atcagcctgg	ccaacatggg	aaaaccagct	tctctactaa	aaatacaaaa	attagctggg	16260
catgggtggg	atcgccctgta	atcccagcta	ctcaggagac	tgaggcatga	gaatcgctta	16320
aaccaagaa	gtggaggttg	cagtgagctg	agatcacgcc	actgcactcc	agcctggggc	16380
acagagtgag	actctgtctc	aaaaaaaaaa	gaaaaaaaaa	tgtaagtga	aaaagttaag	16440
aaaccaaa	aggtttacaa	cactacatga	tttaagcaaa	aaaaattttt	tttgtttttag	16500

agaaagggtc	tcattctgtc	atccaggcag	tgcagtgcga	tcatagctct	ctgcagcctc	16560
aaactcccgg	gttcaagcag	tcctcccgcc	tcagcctctg	gagcagctgg	gactgtaggc	16620
acacaccacc	atgcccagct	aatTTTTTga	TTTTTgtttt	ttgtagagac	ggggtctcag	16680
tatgttgccc	agcctgatct	caaactcctg	gcctcaggtg	atcctcccaa	gtcagcctcc	16740
ccaaagtgct	gggattacag	gcatgtgcc	ccatgctggc	caatTTTTaa	aaatTTTTctg	16800
tagagacagg	gtcttgctat	gttgcccagg	ctggctcttg	actcttgacc	tcaagtgatc	16860
ctgcctcagg	ctcccaaagt	gatgggatta	caggcatgaa	ctaccacacc	tggccttaaa	16920
cttaagcaaa	TTTTTTTTtt	TTTTTggaga	cagtttctact	ctgtcgccca	ggctggagta	16980
aagtggcgtg	atctctgctc	actgcaacct	ccgccccccg	ggtttaagct	attctcctgc	17040
ctcagcctcc	cgagtagctg	ggatataggc	gcctgccacc	acgcctgact	aatTTTTgt	17100
TTTTtagtag	agacgggggt	ttgccatgtt	ggccaggctg	gtctcgaact	cctgacctca	17160
ggcagtccgc	tccccgcac	ccctaccttg	gcctcccaaa	gtgttaggac	tacagggtgtg	17220
agccaccatg	cctggccaaa	TTtaagcaaa	Tgtttgaaaa	cacataccca	caggaatgct	17280
gcacatttta	cccagctact	atgtctaggg	tcgtatctag	cacaccagca	tggctactgt	17340
ggagagctgg	gactggatgt	gagatgagag	ctaaagggga	agtaagcaaa	ccaagcaggg	17400
gaaggtaaga	gaagacagaa	gacagagaga	gagggacct	actctatgag	aggagtccaga	17460
catgtgcaat	tgaaaaagac	ttgctcctgt	ctctcttctg	tgaatgtttg	tgaatatccc	17520
aacgggacac	tttcacagag	gagctgattg	acgtgggtcac	agccatcagc	cttgggacac	17580
cagaccacag	tgtgtacact	aagtggcact	gatggacact	tcagcatccc	tctagctgct	17640
gtcccgtttc	ccctcctcgg	ggaccacagc	tgttgccagt	ccttggtttc	cttcaggagg	17700
gtgtctgggt	agaccagcct	gtgtgcacac	agtccaagat	acatgaacag	tgaagtgcc	17760
ggcaatcctt	gcaagcatgg	gcagggtggag	agctgaggcc	tgcttgacac	cttcctgctc	17820
agaagcccag	tgagcagttt	ccctccctag	ggctcagtg	catcccctat	aaaatggggc	17880
ttatggcaga	gctcaccaca	ctgggtgcat	ctggggattt	ggcgagctca	tgtgcacacc	17940
attgagcatg	gggcccac	tatataaaat	attctacgtc	tgtcagctgc	tgggcactgc	18000
cactatcagc	ctcagtagtg	actgagggac	agggcaccag	tcagagccct	ggtgcacaca	18060
gagtgacccc	agagaagcag	ccttccctct	ctgagtcctg	tttccttctg	ttaggtcctg	18120
acttcatggg	ttgttggttag	cattaaggaa	gtcgctggct	aatTTtatag	tcattgaagt	18180

cagtgggtgtg	caacctgggtt	cctcaaagga	tcacttccct	gaaaaaattc	cactgctccc	18240
tggaggctta	tgcaggccat	cccatcccct	ccctcttggt	gtgttcagct	gacagctttt	18300
tgctcagtga	gtaagtgtta	gggccatttc	acagatgggc	tgcaaccaag	tttgcaagtga	18360
accactaag	accagagcta	gggccaggac	taaatgctgg	tcccaatgcc	acattcccct	18420
gtccccacac	cacatttcct	ccatccggag	accctgttac	cccaacccag	ggccccatta	18480
actccctggc	agaggccctg	ttacatctgc	tgctgccaca	gcctccgccc	acccttcagg	18540
aggcagcagg	tcccactgct	gatgataaag	ttgcaggctg	cctgagctaa	tgaaggggct	18600
tcctctaggc	tgtgcactta	gtcttctgct	tccaaaccaa	atcagaggtg	aggcaccctc	18660
tctgggccc	tctctctcct	ccattttcct	gttgggggtcc	cagggaggaa	gccacttgcc	18720
tagggcccag	gaattttgca	agcctcttgc	cctagggagg	aaggaaggga	ggaggatctt	18780
accttgaact	gtcaagccta	gagcctgggtg	gggcaggcag	aatgggtgc	agtccatgag	18840
ttagaaacac	tagaggagac	actttgctgc	ttggccgggg	caggcaagtt	aattcccag	18900
gctcctgcca	ctgcatctca	atctggaagg	tgaccaggtg	ggcaggaccc	acgtctccca	18960
gatgactcat	tttttctaga	acaggggctt	ggctgccaaa	gaggatactt	gatttcggct	19020
tgtggggaca	gtggtggacc	cagcatctgg	gctttatata	aagggcagct	ttgttgccct	19080
gtaaacacac	agaccatggg	tggccacttc	ttccagtaag	ttagctgggg	agttggaagt	19140
ttaggtaaaa	ccttttgatt	gacaaatgtt	ggcgaattac	catgctgtta	aatgaaacat	19200
tgttctgcca	ccctggggct	gtgggtgcct	gcgtgcaccc	tctgaaaaat	cacacaggaa	19260
gtgggggtggg	gtctctgtga	agctgggtgc	ccccagcctc	agggatgctg	cagaaatgga	19320
atgaggacca	acagggactc	agatgtccaa	ggaagctcta	cagcggagag	gacggcttgg	19380
gaaggaggtc	caggcccagg	tccctccgga	acccaatggg	tatggggcag	cctggctcct	19440
gcctcatccc	ccttctcctg	ttgattgtgt	cctcacagtg	tatgccgccc	gcaaagcagc	19500
cacctcaggt	gttcccagca	tttatgcccc	cagcacctat	gcccacctgt	ctcccgccaa	19560
gacccacccc	ccaccagcta	tgattcccat	gggccctgcc	tacaacgggt	accctggagg	19620
ataccctgga	gacgttgaca	ggagtagctc	aggtgaggcc	gggggaagca	ggaacagctg	19680
gtgggagtgt	gctgggcata	tggacactga	ggggcagggg	ctggaaggaa	gagtgtcttg	19740
ggagccgagg	aggggctctg	ctcctgggtgc	gcggccactg	acagccactc	tccccagct	19800
ggtggccaag	gctcctatgt	accctgctt	cgggacacgg	acagcagtgt	ggcctctggt	19860
gagaatccat	cgtcccgaag	ttggatgtgc	ctgtaaggga	gaggggtggg	ccaggatcca	19920

tcctcccaaa	ccgaccacca	ccccctgtc	cctagaagtc	cgcagtggct	acaggattca	19980
ggccagccag	caggacgact	ccatgcgggt	cctgtactac	atggagaagg	agctggccaa	20040
cttcgaccct	tctcgacctg	gcccccccag	tggccgtgtg	gagcggggta	agcaggagcc	20100
ttgggggtctg	agggctttta	aggtgggggg	gtgaaacatg	tctccctgat	acctgccgca	20160
gggactcttg	gtgcaaacc	tggaccccgg	gctcctccag	cagtcagtga	cacccccctt	20220
ccctgcagcc	atgagtgaag	tcacctccct	ccacgaggac	gactggcgat	ctcggccttc	20280
ccggggccct	gccctcacc	cgatccggga	tgaggagtgg	ggtggccact	ccccccggag	20340
tcccagggga	tgggaccagg	agcccggccag	ggagcaggca	ggcgggggct	ggcggggccag	20400
gcggccccgg	gcccgctccg	tggacgccct	ggacgacctc	accccggcca	gcaccggcca	20460
gtcagggagc	aggtctccca	cgagtaatgg	tgggagaagc	cgggcctaca	tgcccccgcg	20520
gagccgcagc	cgggacgacc	tctatgacca	agacgactcg	agggacttcc	cacgctcccg	20580
ggacccccac	tacgacgact	tcaggtctcg	ggagcgccct	cctgccgacc	ccaggtccca	20640
ccaccaccgt	acccgggacc	ctcgggacaa	cggctccagg	tccggggacc	tcccctatga	20700
tgggcggtta	ctggaggagg	ctgtgaggaa	gaaggggtcg	gaggagagga	ggagacccca	20760
caaggaggag	gaggaagagg	cctactacce	gcccgcgccc	ccccgtact	cggagaccga	20820
ctcgcaggcg	tcccagagagc	gcaggctcaa	gaaggtgagg	gccgccctcc	ctggcggtcca	20880
gaccgtccct	gggccccccag	ccggtccccg	cggctcatac	ccttctttct	ttctcccttg	20940
cagaacttgg	ccctgagtcg	ggaaagttaa	gtcgtctgat	ctgacgtttt	ctacgtagct	21000
tttgtatttt	tttttttaat	ttgaaggaac	actgatgaag	ccctgccata	cccctcccga	21060
gtctaataaa	acgtataatc	acaagctctg	gagagaacca	tttgttcggc	cgcgcggggc	21120
gggggaccgg	ggctgctccc	gtatgcgtct	gtaaagcgcc	gcgtcccggg	ggcaccggag	21180
tccggggccg	ggaggaagag	accagcctg	gcccggcccc	cgcccgcgcc	gccggccgga	21240
gaacgtgccc	cgcgcagccg	ccgcccgcct	gcgtgcgcgc	cccggccccg	cccaggcgtg	21300
cgcattgcgc	ccggccctcc	gccttcgcgc	accgcaggct	ggcgtccggg	gacgcgcgcg	21360
cgtcctctc	cccttcagc	ccatcccccc	cagcccccca	ccgacctact	ttactgtctc	21420
caaactcggg	cagcccacct	ggcccccgac	gaccccagcc	cctgcaccgg	gtacccccgac	21480
gttccatcca	gaccgcggtt	tcaccagggc	ggcgcgcggc	gacctcgcgc	cccgcggagc	21540
cccgggctcg	cgcgcgcccc	cccggccccg	gagacagacc	agcgcgcgcg	ccccgggccg	21600

cctcccccca gcgcgcgtcc gccccggggc tcgcgccgcc gccgccgccg ccgccgcgcg 21660
cgcgagctc aagtaaagga ggaaaaaaaa aagggggaaa aatagaaagc ggcggcggct 21720
gcagcagcga tccgccgccg gactgggcca agccggggcg cggccgcgcg agccggcgat 21780
ccagggcact ggcggcggcc agccagggcg ggccgtgttc aaaaaaaaaa gtcgcggcg 21840
cggcggtgc tcagggaagg aggcctgagg gccgcgtgca gcgggcgggc agctgggtgg 21900
gctggggggcg gccgcgcggc gtcccggagc ctggggccgc ccggagccgg cgggcgggcg 21960
gaggcggagg cggcggcggc tgcagcggct gcaggagcgg cggcggtgc ggcggcggcg 22020
gcggcatctc ctctcacat gacccactg tttgtccccg tgatcagcgc gagcggctcc 22080
cgtatctcct ccgtcccctc ctgccgcgcg gcgtgagcgc cgggctcggg gcccccccg 22140
ccgccgccc cctcccctcc ctccctcccc tcccctcccc tcccccccg gccccgcgc 22200
cccccgccc ccgccccccc catggacatg ctggaccgg gtctggatcc cgctgcctcg 22260
gccaccgctg ctgccgcgc caggtaagat ccccgccccg gccgtgcccc cgcgcccccg 22320
ccccggcccc ggccccgcgg cctgcaggcc ggggcccga tgatcccag cggccgcggg 22380
cccggctcaa aatggaggcc gccggcgcg gggggacctg gcgcctccc cccccggccc 22440
ccggcctcgg cggcgcccc ggccctcaggc gcggccgggt gggactgggg ccctgcagct 22500
gggcgcgggg gcggggggcg gggcgcgggc cgcgctgacc ctgctccctc ctgtgcccct 22560
ggcagccacg acaagggacc cgaggcggag gagggcgtcg agctgcagga aggtgagtgc 22620
ttgccggggc ggccgcgccc ggggagggt gggggcgctc ggcgcgggcc tgaccgtgcc 22680
ccgaccctcc tcggccccag gcggggacgg cccaggagcg gaggagcaga cagcgggtggc 22740
catcaccagc gtccagcagg cggcgttcgg cgaccacaac atccagtacc agttccgcac 22800
agagacaaat ggaggacagg tgagcggcg gccgcgagg cgaacgggcg ggcgggcggg 22860
cgcgccggga aggtcggac ctggccccag cgccggcctc gccgctctgc cggccccctgc 22920
aggtgacata ccgcgtagtc caggtgactg atggtcagct ggacggccag ggcgac 22976

<210> 20
<211> 30
<212> DNA
<213> Rattus norvegicus

<400> 20
gttacagaat tcgccgcgat ggccggcg

30

<210> 21
<211> 20
<212> DNA
<213> Rattus norvegicus

<400> 21
gccaggacag tgtacgcact 20

<210> 22
<211> 20
<212> DNA
<213> Ratus norvegicus

<400> 22
acctcaggtg tcccgagcat 20

<210> 23
<211> 20
<212> DNA
<213> Rattus norvegicus

<400> 23
gaagatgact ggcgatcgag 20

<210> 24
<211> 20
<212> DNA
<213> Rattus norvegicus

<400> 24
acctctatga cccggacgat 20

<210> 25
<211> 20
<212> DNA
<213> Rattus norvegicus

<400> 25
caccaccctg acagtgcgta 20

<210> 26
<211> 20
<212> DNA
<213> rattus norvegicus

<400> 26
ctgggggcat agatgctcgg 20

<210> 27
<211> 20
<212> DNA
<213> Rattus norvegicus

<400> 27
gccctggaag gcctcgatcg 20

<210> 28
<211> 20
<212> DNA
<213> Rattus norvegicus

<400> 28
caagtccta ggatcgatccg 20

<210> 29
<211> 20
<212> PRT
<213> Rattus norvegicus

<220>

<221> Misc_Feature
<222> 169..188
<223> Position in SEQID2

<400> 29
Ser Ala Gln Asp Leu Asp Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile
1 5 10 15

Val Leu Gly Arg
20

<210> 30
<211> 15
<212> PRT
<213> Rattus norvegicus

<220>

<221> Misc_Feature
<222> 556..570
<223> Position in SEQID2

<400> 30
Glu Glu Gly Gln Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr
1 5 10 15

<210> 31
<211> 21
<212> DNA
<213> Homo sapiens

<400> 31
atgcaacagg acggacttgg a

21

<210> 32
<211> 28
<212> DNA
<213> Homo sapiens

<400> 32
tcagacgact aaactttccc gactcagg

28

<210> 33
<211> 20
<212> DNA
<213> Homo sapiens

<400> 33
ctacaacccc tacgttgagt

20

<210> 34
<211> 24
<212> DNA
<213> Homo sapiens

<400> 34
tcgtgacctg acctttgacc agac

24

<210> 35
<211> 24
<212> DNA
<213> Homo sapiens

<400> 35
cctgagctac tcctgtcaac gtct

24

<210> 36
<211> 20
<212> DNA
<213> Homo sapiens

<400> 36
aggccgagat cgccagtcgt

20

<210> 37
<211> 27
<212> DNA
<213> Homo sapiens

<400> 37
ctacatggat ccagtcatgc cgaagat

27

<210> 38
<211> 28
<212> DNA
<213> Homo sapiens

<400> 38
cgacaactcg agtcagttgg tatcatgg

28

<210> 39
<211> 15
<212> PRT
<213> Homo sapiens

<220>

<221> Misc_Feature
<222> 1..14
<223> Identical to 5 .. 18 in ref swissprot :Q07021

<400> 39
Leu Arg Cys Val Pro Arg Val Leu Gly Ser Ser Val Ala Gly Tyr
1 5 10 15

<210> 40
<211> 16
<212> PRT
<213> Homo sapiens

<220>

<221> Misc_Feature
<222> 2..15
<223> Identical to 268 .. 282 in ref swissprot :Q07021

<400> 40
Cys Tyr Ile Thr Phe Leu Glu Asp Leu Lys Ser Phe Val Lys Ser Gln
1 5 10 15

<210> 41
 <211> 21721
 <212> DNA
 <213> Homo sapiens

 <220>

 <221> exon
 <222> 1898..2253

 <221> exon
 <222> 3438..3782

 <221> exon
 <222> 12064..12183

 <221> exon
 <222> 15049..15105

 <221> exon
 <222> 15670..15816

 <221> exon
 <222> 19486..19659

 <221> exon
 <222> 19806..19865

 <221> exon
 <222> 19963..20094

 <221> exon
 <222> 20236..20864

 <221> exon
 <222> 20954..21094

 <221> Misc_Feature
 <222> 715
 <223> diverging nucleotide, G in ref genbank:AC002128

 <221> Misc_Feature
 <222> 1229
 <223> diverging insertion, G in ref genbank:AC002128

 <221> Misc_Feature
 <222> 3676
 <223> diverging nucleotide, T in ref genbank:AC002128

 <221> Misc_Feature
 <222> 5039
 <223> diverging deletion, G in ref genbank:AD000684

 <221> Misc_Feature
 <222> 5118

<223> diverging nucleotide, C in ref genbank:AD000684

 <221> Misc_Feature
 <222> 7337
 <223> diverging deletion, C in ref genbank:AD000684

 <221> Misc_Feature
 <222> 8294
 <223> diverging nucleotide, G in ref genbank:AD000684

 <221> Misc_Feature
 <222> 8604
 <223> diverging nucleotide, C in ref genbank:AD000684

 <221> Misc_Feature
 <222> 8928
 <223> diverging nucleotide, A in ref genbank:AD000684

 <221> Misc_Feature
 <222> 9021
 <223> diverging nucleotide, G in ref genbank:AD000684

 <221> Misc_Feature
 <222> 9851
 <223> diverging insertion, GAATGAAA in ref genbank:AD000684

 <221> Misc_Feature
 <222> 9878
 <223> diverging nucleotide, C in ref genbank:AD000684

 <221> Misc_Feature
 <222> 11478
 <223> diverging nucleotide, T in ref genbank: AD000684

 <221> Misc_Feature
 <222> 11577
 <223> diverging deletion, C in ref genbank:AD000684

 <221> Misc_Feature
 <222> 11779
 <223> diverging nucleotide, T in ref genbank:AD000684

 <221> Misc_Feature
 <222> 13411
 <223> diverging deletion, T in ref genbank:AD000684

 <221> Misc_Feature
 <222> 13538
 <223> diverging nucleotide, G in ref genbank:AD000684

 <221> Misc_Feature
 <222> 13896
 <223> diverging nucleotide, G in ref genbank:AD000684

 <221> Misc_Feature
 <222> 14912
 <223> diverging nucleotide, A in ref genbank:AD000684

<221> Misc_Feature
 <222> 16732
 <223> diverging nucleotide, C in ref genbank:AD000684

<221> Misc_Feature
 <222> 17169
 <223> diverging nucleotide, G in ref genbank:AD000684

<221> Misc_Feature
 <222> 18946
 <223> diverging deletion, G in ref genbank:AD000684

<221> Misc_Feature
 <222> 19474
 <223> diverging nucleotide, G in ref genbank:AD000684

<221> Misc_Feature
 <222> 20500
 <223> diverging deletion, G in ref genbank:AD000684

<221> Misc_Feature
 <222> 20501
 <223> diverging deletion, G in ref genbank:AD000684

<221> Misc_Feature
 <222> 20502
 <223> diverging deletion, A in ref genbank:AD000684

<221> Misc_Feature
 <222> 21270
 <223> diverging nucleotide, G in ref genbank:AD000684

<221> Misc_Feature
 <222> 21356
 <223> diverging insertion, T in ref genbank:AD000684

<221> Misc_Feature
 <222> 21476
 <223> diverging nucleotide, A in ref genbank:AD000684

<221> Misc_Feature
 <222> 21588
 <223> diverging insertion, C in ref genbank:AD000684

<221> Misc_Feature
 <222> 21601
 <223> diverging deletion, T in ref genbank:AD000684

<221> Misc_Feature
 <222> 21635
 <223> diverging insertion, G in ref genbank:AD000684

<221> Misc_Feature
 <222> 19963..19965
 <223> Potential variant splicing site AAG

<221> Misc_Feature

<222> 1..21721

<223> n= a,g,c or t

<400> 41

aacagtttgg cagttcctca aaagggttaaa aatagaacta ccaagtcacc cagcaattcc	60
attcttaggc atatattcaa aagaaatgaa agcagatatt tgtacaccag tgttcacagc	120
tgcactattt acaatagtca aaaggtagaa acaacctagg tccatccaca aatgaatgga	180
taaataaaac gtagcatata catacaatgg tacactagtc cgctgtaaaa agaaattttg	240
atcttactgc atgctacatg gcttcgacat actacaacat ggatggacct tgaaaacatt	300
attctttgtg aaataaacta gacacaggac aaatgtaga cgattccact tatatgaggc	360
acctagaatg ggcaatttgg taagcaaagt agaatagaaa ttactagggg cacaggtagc	420
agggaaatggg gagttactgt ttaatgggtca cagagtttat gttggggatg atgaaacagt	480
ttcggggata aagagtgggtg actggtacac gacattgtga atatacttaa tgccactgaa	540
ttttacactt gaagtgggtta aagcgataaa tattatagnt ttgcatattt tatcataaaa	600
atatTTTTTT aaacgatgaa gggacgtgaa cgggttgaaa ttttataaaa agtggccagg	660
gaagggtgtca ctgcaatggg gtcctacagg aggaggaaga tcatgtggac atctccggga	720
aggggtgttct ggcagagggg gtagcacggg cgatggctct gaggactgtg agaagtatag	780
ttggaaacag cgaggaggcc aggggtgtccg aagctgagta agccagagag agtgggagga	840
ggtgagataa gagggggaag gtcagtttct gctgagagtg aggaggagcc acaggagggc	900
tgtgagcagg tggacgtgat ctggcttgag ttttaacagg gccagtagaa caaagcacgc	960
ctgggtaccg aaaccagcca ctggccagtt ggcaacctgg gggagtctaa cgcgaggaag	1020
cgcccagggt tccccagga tgcgctttcc ctcgccgcca cctggagaca gcagagtcac	1080
gccagcgtc ggcagggctg atcgccgcgc cgcgcccccg ccctcggctc caggtggctc	1140
gttccgggaa ttcctaagcg gaaaccggtc ccaagccccg cgccttcgct cggccccttt	1200
aagagccaga atttccggag ggctgacctg gggctaggga tgcccagggg ccgaaccaca	1260
agttgggaac ggggtggggg ggtggcgaaa acttccgaag tggaattcca acttttcctg	1320
gccctgattc cccttgggca tccctgangg ggcagagctt cccttcggg gacttttagag	1380
ggttcctcag gtcattctaac tgggagacac aggaggcccc aagcgcccc cctccacccg	1440
gtccggagga accccagtgg aagtggagaa gtcaggcgcc accaacaagc ctctcccagc	1500
caggactttg cttagactcg ctcctcccgg cagggcgcac ctaggcgggt ccatcgccag	1560

ccggggagag	gggtttgggc	agggagggaa	caggtgcgcg	gcgggacccg	ccctatctca	1620
acaggtgaat	cgctccaagt	gggtctcggt	tgcattggatc	tcgggtgcgc	tggtttggcc	1680
ggagcagatg	ggggccggaa	gggacctgtg	gtccgcaggc	gccctcccag	cgggccagtc	1740
acttggttcg	ggccctgggg	gacggagcgc	acctgggtca	gccacttcc	ggggagggag	1800
gcagaggaac	ccctccccgc	cgctcacccc	taagcccagc	cctcggctcc	cacccttgtg	1860
tacctgggcc	gaaccattca	ccggagcgcg	cagcgggtgg	agtgtggctc	ggaggaccgc	1920
ggcgggtcaa	gcacctttct	ccccatatc	tgaaagcatg	ccctttgtcc	acgtcgttta	1980
cgctcattaa	aacttccaga	atgcaacagg	acggacttgg	agtagggaca	aggaacggaa	2040
gtgggaaggg	gaggagcgtg	cacccctcct	ggccttgggtg	cgcgccgcgc	cccctaaggt	2100
actttggaag	ggacgcgcgg	gccagacgcg	cccagacggc	cgcgatggcg	ctgttggccg	2160
gcgggctctc	cagagggctg	ggctcccacc	cggccgcccgc	aggccgggac	gcggtcgtct	2220
tcgtgtggct	tctgcttagc	acctgggtgca	caggtacggg	gcacggggcc	tctgacgctg	2280
cggaacgccg	gagggaaactg	tagaggggga	tggatggagt	tggaggcggc	gggaagcggg	2340
aagcgggggt	ctcagaggct	gggaccttcc	gatcccctgg	gtcttgggcg	atctgttgcg	2400
ncgcggggagt	gagaggaatt	ccccatttgt	gccggggagc	gctccccgcg	cccttatctg	2460
gaagatagca	ggaagtgaaa	ctccctggac	ggtgagacct	ggagcggcag	ggagaatgga	2520
actctttgtg	gggagggagt	ggaagaccgc	ccgatctctg	ggaaaagaaa	agccgggatg	2580
ggacttgggc	gcacccgggg	atttctaagt	tttgagtaga	cggggagagg	gcacgggagg	2640
gctggatcag	acgcttccta	gagggacaga	gacgaaggaa	caatgcctag	gcctcgggtg	2700
ggtgtgggac	tggggactcc	ccatcccccg	cacccacccc	acctcccgcg	ggctccggat	2760
tatacgtgcg	taagagtctg	gtgggatgga	tttacggact	tgaaaccgac	ttctgctggc	2820
aggctttcac	ctggatggga	tatttgggtg	gtgatgaggt	ctttcccagag	acacttttgg	2880
ttcagtcatt	tgaaatgact	ttagagtagg	gtgaggtggt	gggaggctga	tggagatatt	2940
gtgggggctt	tagtccctcc	atggcaaagc	agttcaggca	aacaactcca	tggttttccc	3000
tccaaattca	aaaggccccg	ggtaacctgg	aatccttcgt	agtcggtttt	gaagtggggc	3060
cttgggcgct	gggggcatca	acatggccat	ctgggcttgc	ctgcccaggc	cacacagagg	3120
ccccttgttg	tgggtgaatg	gcaaagggaa	gaggggactg	gtgtggttca	gaggccacag	3180
gctgggaaga	gggatggcgg	gcgagtccaa	ggaaactggc	cgtgtcaccg	tgcacctgcc	3240
acttcagccc	cacgggtcta	taaaatgggc	atgattatcg	tggctacctc	actggtcctg	3300